STIC-Biotech/ChemLib

100981

Fr m: Sent:

Baum, Stuart

To: Subject: Friday, August 08, 2003 4:35 PM STIC-Biotech/ChemLib

Sequence Search....thank you

Please do a standard and interference sequence search for:

(1) SEQ ID NO:78 (2) DNA's that encode SEQ ID NO:78

EXAMINER # 78896 DATE:8/8/2003

SERIAL NUMBER:09/921992

MAIL BOX ROOM: CM1 9E12 OFFICE ROOM # CM1 9D06

RESULTS FORMAT: PAPER

THANKS...Stuart

Stuart F. Baum Ph.D Art Unit 1638 CM1 9D06 (703) 305-6997 stuart.baum@uspto.gov

Edward Hart Technical Info. Specialist STIC/Biotech

CMI 6B02 Tel: 305-9203

Searcher:
Phone:
Location:
Date Picked Up: X/1/07
Date Completed:
Searcher Prep/Review:
Clerical:
Online time:

TYPE OF SEARCH:
NA Sequences:
AA Sequences:/
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

VENDOR/COST (where applic.)
STN:
DIALOG:
Questel/Orbit:
DRLink:
Lexis/Nexis:
Sequence Sys.: (())
WWW/Internet:
Other (specify):



STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 100781

TO: Stuart Baum

Location: CM-1/9D06/9E12

Art Unit: 1638

Friday, August 15, 2003

Case Serial Number: 09921992

From: Edward Hart

Location: Biotech-Chem Library

CM1-6B02

Phone: 305-9203

edward.hart@uspto.gov

Search Notes

Examiner Baum,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart



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STIC SEARCH RESULTS

Biotech-Chem Library

Questions about the scope or the results of the search? Contact the searcher or contact:

Mary Hale, Information Branch Supervisor 308-4258, CM1-1E01

Vo	luntary Results Feedback Form
>	I am an examiner in Workgroup: Example: 1610
>	Relevant prior art found, search results used as follows:
	☐ 102 rejection
	☐ 103 rejection
	☐ Cited as being of interest.
	☐ Helped examiner better understand the invention.
	Helped examiner better understand the state of the art in their technology.
	Types of relevant prior art found:
4	☐ Foreign Patent(s)
	Non-Patent Literature
<i>K</i>	(journal articles, conference proceedings, new product announcements etc.)
	Relevant prior art not found:
	Results verified the lack of relevant prior art (helped determine patentability).
	Results were not useful in determining patentability or understanding the invention.
on	nments:

Droploff or send completed forms to STIC/Biotech Chemilibrary CM1=Circ+Desk



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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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33109327

ALIGNMENTS

RESULT 1 AAB45692 ID AAB4

AAB45692 standard; Protein; 372 AA.

15-MAR-2001 (first entry)

AAB45692;

E. coli gcpE protein. WPI; 2001-025196/03. N-PSDB; AAC82653. 20-MAY-2000; 2000WO-EP04592. Isoprenoid; gcpE; yfgB; anti
antimycotic; antiparasitic; Incorporating gcpE and yfgB genes into viruses and cells, for Jomaa H; 21-MAY-1999; 21-MAY-1999; 30-NOV-2000. WO200072022-A1 Escherichia coli. (JOMA/) JOMAA H 99DE-1023567. 99DE-1023568. antimicrobial; transgenic plant; agriculture; tic; antiviral; fungicidal; herbicidal.

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    gcpE gene; methyl-D-erythmitol phosphate; MEP; dimethylallyl diphosphate; transgenic plant; isoprenoid compound; tocopherol; isoprentyl diphosphate; food; feed source; transfection; single nucleotide polymorphism; SNP; oxidative stress tolerance; UV tolerance; transformation; GCPE protein;
                                                                                                    Escherichia
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                          AADPVEEIKVGFDILKSLRIRSRGINFIACPTCSRQEFDVIGTVNALEQRLEDIITPMDV
                                            AADPVEEIKVGFDILKSLRIRSRGINFIACPTCSRQEFDVIGTVNALEQRLEDIITPMDV
                                                                                                                        KASDVFLAVESYRLLAKQIDQPLHLGITEAGGARSGAVKSAIGLGLLLSEGIGDTLRVSL
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                                                                                                    KASDVFLAVESYRLLAKQIDQPLHLGITEAGGARSGAVKSAIGLGLLLSEGIGDTLRVSL
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Conservative

0;

Mismatches

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Indels

0

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180

120 120

240 180

300 240

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The invention relates to gcpE nucleic acid molecule, an essential gene confinethyl-D-erythritol phosphate (MEP) pathway) that encodes rice, arabidopsis thaliana or Escherichia coli GCPE protein. gcpE is useful CC canola, castor bean, coconut, cotton, crambe, linseed, maize, mustard, coli palm, peanut, rapeseed, rice, safflower, sosphan, sunflower, cc or wheat with an increased isoprenoid (tocopherol) compound level. The CC expression of GCPE protein in organisms increases the level of cc expression of GCPE protein in organisms increases the level of cc expression of GCPE protein in organisms overexpressing GCPE CC diphosphate biosynthesis. Transgenic organisms overexpressing GCPE CC protein can nutritionally enhance food and feed sources. Overexpression of GCPE protein in transgenic plant may provide tolerance to stresses CC e.g., oxidative stress tolerance such as to oxygen or ozone, UV tolerance, etc. gcpE may be used to obtain nucleic acid molecules from CC the same species, and to obtain nucleic acid homologues. gcpE is also used to ransfection. gcpE an also act as markers capable of CC detecting polymorphisms such as single nucleotide polymorphisms (SNPs). gcpE is also used to determine the level or pattern of expression of the protein. The present sequence is Escherichia coli GCPE protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gcpE nucleic acid which is an essential gene of the methyl-D-erythritol phosphate pathway, encoding a fully defined GCPE protein which is useful for increasing levels of tocopherol substrates in plants -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-AUG-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 155pp; English.
Score 1866; DB 23; pred. No. 7.6e-181;
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                                    Length
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Seeman

Best Local Similarity

49.2%;

Pred.

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                                                                                                            monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein encoded by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, an for blosynthesis and biodegradation, especially biosynthesis of Vitamin B12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes-related diseases. In addition, the genome sequence and proteins encoded by it are discussed to the genome sequence and proteins encoded by it are useful in pharmaceutical and
                                                                                                                                                                                                                                                                             The present invention relates to the genome sequence of Listeria monocytogenes EGD-e (see ABAO3041). The genome sequence and fragrit are useful for selecting probes and primers for detecting genomonocytogenes and related organisms, and for studying genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
                                               Note: The sequence data for this patent did not specification, but was obtained in electronic
                                                                                 vaccines compositions for the treatment or prevention monocytogenes and related organisms.
                                                                                                                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                                                                                               Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P, Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart Daniels J, Goabel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA; Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A, Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L; Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N; Berche P, Charbit A, Durant L; Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N; Maddenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation; vitamin Bl2; bacterial infection; disease.
                                                                                                                                                                                                                                                                                                                                                                                                     related
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                              itp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                  SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Voss
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                                                                                                                                                                                                                                                                                                                                                                  No 663;
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                                                                                                                                                                                                                                                                                                                                                               192pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               368
                                                                                                                                                                                                                                                                                                                                                                  French.
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Match

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Score

868;

DB

23;

Length

% identity or which hybridises with the sequences given and ABQ81843. Also described is a polynucleotide (II) e protein, comprising a sequence selected from 1097 seque

encoding

368

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IBB965
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                                The present invention describes a polynucleotide (I) comprising a sequence of a Bifidobacterium genome selected from the nucleotide sequences given in ABO81842 and ABO81843, or a sequence exhibiting at
                       sequences given in
least 90% identity
                                                                                      Claim
                                                                                                         Novel polynucleotide comprising Bifidobacterium genome sequence useful as a probe or primer for detecting and/or identifying Bifidobacterium longum in a biological sample \,
                                                                                                                                                                                                                                                                                                                                                                  Bifidobacterium longum NCC2705; antidiarrheic; antibacterial; ir
                                                                                                                                                                                                                                                                                                                                                                                                     Bifidobacterium longum NCC2705 ORF amino acid sequence SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABP65322;
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                                                                                                                                                                                                                                        30-JAN-2001; 2001EP-0102050
                                                                                                                                                                                                                                                                                          EP1227152-A1
                                                                                                                                                                                                                                                                                                                   Bifidobacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABP65322 standard;
                                                                                                                                                                                                                                                                                                                                                   identification;
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                                                                                    SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GPGEALVSTLGVTGGNKKSGLYEDGVRKDRLDNNDMIDQLEARIRAKASQLDEARRIDVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KVGFDILKSLRIRSRGINFIACPTCSRQEFDVIGTVNALEQRLEDIITPMDVSIIGCVVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIPIRIGVNAGSLEKKIIQKYGYPTADGMVESALAHIKILEDLDFYDIIVSLKASDVNLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIPIRIGVNAGSLEKDLQEKYGEPTPQALLESAMRHVDHLDRLNFDQFKVSVKASDVFLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RENTRPVQVGNLTIGGSEELTIQSMTTTKTHDVEATVAEIHRLEEAGCQIVRVACPDERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RKSTR-IYVGNVPIGDGAPIAVQSMTNTRTTDVEATVNQIKALERVGADIVRVSVPTMDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GPGEAREADIGIAGSNGEGLLFRHGKIIRKVPEAIMIDELKKEIDILAEEF-FVKKIDLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KVAREVLKSFGLSSNAAMLISCPTCGRIEIDLIRIANEVENYIAKIEVPIKVAVLGCAVN
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                                                                                 ID 66; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                               (first
                                                                                                                                                                                                                                                                                                                longum.
                                                                                                                                                                                                                                                                                                                                        composition; pharmaceutical
                                                                                                                                                                                                                                                                                                                                                      lactic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein;
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                                                                                                                                                                                                                                                                                                                                                   acid bacterium; diarrhoea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                403
                                                                                                                                                                                                                                                                                                                                                                  inhibitor of Salmonella;
                                                                                                                                                                                                                                                                                                                                                                            Bifidobacterium;
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smatches 115;
                                                                                                                                                                                                                                                                                                                                        composition
                                                                                                                                                                                                                                                                                                                                                                              bacterial;
                                                                                                                                                                                                                                                                                                                                                     pathogenic
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                                                                                                                                                                                                                                                                                                                                                                  detection;
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                                                                                                                                                                                                                                                                                                                                                     bacteria;
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RESULT 5
AAW98298
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibacterial activities,
(I) (which is a probe) is
of Bifidobacterium longum
the lactic acid bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pathogenic bacteria and/or
selected from milk, yogurt
fermented products, ice-cre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 given in ABP65258 to ABP66 encoding a heterologous po
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               can be used for preventing
W09843478-A1.
                                                                    GHPO protein;
peptic ulcer
                                                                                                                                                                31-MAR-1999
                                                                                                                                                                                                                                        AAW98298 standard; Protein)
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                                  Helicobacter
                                                                                                                                                                                                      AAW98298
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                                                                                                                          pylori
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                                  pylori.
                                                                                                                                                                (first entr
                                                                                       Helicobacter infection; gastroduodenal disease;
                                                                                                                             76
                                                                                                                           protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70;
                                                                                                                                                                                                                                                                                                                                                                                                       EGVASGNGKGQIFIKGKVIKTVPEDQIVDTLLTIANDIAAQME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        this patent on sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                           GVTGGNKKSGLYEDG-----VRKDRLDN-----NDMIDQLE
                                                                                                                                                                                                                                        359
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Pred. No. 8.4e-74;
                                                                                                                                                                                                                                        A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        is not represented in the printed information supplied by the
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                                                                                         gastritis;
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                                                                                                                                                                                                                                                                                                                                                                                                          381
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SAPHO syndrome; Propionibacterium

synovitis;

acne;

pustulosis;

hypertosis; osteomyelitis;

acnes immunogenic protein #17108

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RESULT 6
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Best Local
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01-APR-1997;
24-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention. The polypeptides can be used for preventing or treating Helicobacter infections, and gastroducdenal diseases associated with these infections, including acute, chronic, and atrophic gastritis, and peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also be used for the production of antibodies. The products can also be used for detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents a Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 8; Page 372-374; 2054pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated Helicobacter polynucleotides for the diagnosis, prevention and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-542293/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Al-Garawi A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC.
(INMR) MERIEUX ORAVAX PASTEUR
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                                                 27-FEB-2002
                                                                          AAU56212;
                                                                                                 AAU56212 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               infections and gastrointestinal
                                                                                                                                                                                                               243
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                                                                                                                                                             ALGEAKHADMATAFGNRSGLTIKEGKVIHKLAEKDLFETFVIEVENLAKEREKS
                                                                                                                                                                                                                                                                                                                               NIPIRIGVNAGSLEKDLQEKYGEPTPQALLESAMRHVDHLDRLNFDQFKVSVKASDVFLA 188
                                                                                                                                                                                                                                                                                                                                                                                                                             RRKSTRIYVGNVPIGDGAPIAVQSMTNTRTTDVEATVNQIKALERVGADIVRVSVPTMDA
                                                                                                                                                                                      GPGEALVSTLGVTGGNKKSGLYEDGVRKDRLDNNDMIDQLEARIRAKASQLDEA
                                                                                                                                                                                                                                                                            VESYRLLAKQIDQPLHLGITEAGGARSGAVKSAIGLGLLLSEGIGDTLRVSLAADPVEEI
                                                                                                                                                                                                                                                                                                               NIPIRIGVNAGSLEKQFDQKYG~PTPKGMVESALYNAKLLEDLDFTNFKISLKASDVIRT
                                                                                                                                                                                                                                                                                                                                                               AEAFKLIKQQVNVPLVADIHFDYRIALKVAEYGVDCLRINPGNIGNEERIRMVVDCARDK 128
                                                                                                                                                                                                               KVARAILRHSGRLKEGINWISCPTCGRIEANLVDMAIKVEKRLSHIKTPLDISVMGCVVN
                                                                                                                                                                                                                                     KVGFDILKSLRIRSRGINFIACPTCSRQEFDVIGTVNALEQRLEDIITPMDVSIIGCVVN
                                                                                                                                                                                                                                                                IEAYRMLRPLVIYPFHLGVTEAGNLFSSSIKSAMALGGLLMEGIGDTMRVSITGELENEI
                                                                                                                                                                                                                                                                                                                                                                                                                  RVKTKQIFIGGVAIGGDAPISTQSMTFSKTADIESTKNQIDRLKLAGADLVRVAVSNEKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kleanthous H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97US-0902615.
97US-0833457.
97US-0881227.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
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                                                 entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42.6%;
                                                                                                   415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 794; DB 19;
Pred. No. 8.5e-72;
3; Mismatches 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Miller C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MERIEUX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diseases
                                                                                                   Å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SERUMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pylori GHPO protein for preventing or +-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oomen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           used to develop
of Helicohart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ₽₽,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         products
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     c P. acnes. The disorders include SAPHO syndrome (synovitis, acne, C pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. C P. acnes is also involved in infections of bone, joints and the central centrous system, however it is particularly involved in the inflammatory c lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention c and determining the amount of bound protein in the sample. The c polypeptides may be used as antigens in the production of antibodies c specific for P. acnes proteins. These antibodies can be used to c downregulate expression and activity of P. acnes polypeptides and c therefore treat P. acnes infections. The antibodies may also be used as c diagnostic agents for determining P. acnes presence, for example, by c enzyme linked immunosorbent assay (ELISA).

C Note: The sequence data for this patent did not form part of the printed constraints of 
                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-APR-2000;
02-JUN-2000;
07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequences AAU39105-AAU68017 represent Propionibacterium acnes polypeptides. The proteins and their associated DNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Propionibacterium acnes vaccinating against and treating acne vulgaris .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L'maisonneuve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Propionibacterium acnes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 uveltis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-APR-2001; 2001WO-US12865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dermatólogical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The proteins and their associated DNA sequences treatment, prevention and diagnosis of medical conditions acnes. The disorders include SAPHO syndrome (synovitis, acrestings, hyperstates) acres.
        233
                                             188
                                                                                                                                 128
                                                                                                                                                                          113
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                                                                                                                                                                                                                                                         53
                                                                                                                                                                                                                                                                                                                                                            Similarity
                 KNIPIRIGVNAGSLEKDLQEKYGEPTPQALLESAMRHVDHLDRLNFDQFKVSVKASDVFL
                                                                                                                                                             AEVLPIIAKRSQIPVIADIHFQPKYVFQAIEAGCGAVRVNPGNIRKFDDQIESICQAATE
MIRAYEQLAAKCDYPLHLGVTEAGPAFQGTIKSAVAFGHLLAEGIGDTIRVSLSADPVEE
                                                                            HGTSIRIGVNAGSLDKRLLDKYGAPTAEAMVESALWEASLFEQYGFRDFKISVKHHDPVV
                                                                                                                                                                                       AEAFKLIKQQVNVPLVADIHFDYRIALKVAEYGVDCLRINPGNIGN-EERIRMVVDCARD 127
                                                                                                                                                                                                                                            RRKSTRIYVGNVPIGDGAPIAVQSMTNTRTTDVEATVNQIKALERVGADIVRVSVPTMDA
                                                                                                                                                                                                                                                                                                                                                                                                                           415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID No 17407;
                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; 2000US-199047P.
; 2000US-208841P.
; 2000US-216747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Persing
e J, Zha
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                                                                                                                                                                                                                                                                                                                                                            42.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptides and nucleic acids useful for diagnosing infections, especially useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mitcham JL, Wang
, Jen S, Carter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1069pp;
                                                                                                                                                                                                                                                                                                                                                         Score 785.5; DB
Pred. No. 7.9e-7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neuroprotectant.
                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wang SS,
arter D;
                                                                                                                                                                                                                                                                                                                                                                           DB 22;
                                                                                                                                                                                                                                                                                                                                      132;
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                                                                                                                                                                                                                                                                                                                                                                           Length
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s are used in
s caused by
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292
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G 9

RRKSTRIYVGNVPIGDGAPIAVQSMTNTRTTDVEATVNQIKALERVGADIVRVSVPTMDA

RRKTRQLMVGKVGVGSDHPISVQSMTTTKTHDINGTLQQIAQLTATGCDIVRVACPKTVD

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RESULT 7
AAAG91951
ID AAG9
XX AAG9
AC AAG9
AC AAG9
AC COT
XXX COT
XXX COT
XXX COT
XXX ID-1
PN EP1
XXX ID-1
PN 07-7
PR 
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           Matches
                                                            Query Match
                                                                                                                                                                        The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-DEC-1999;
07-APR-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nakagawa
Tateishi
                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 17; SEQ ID NO: 5705; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-376931/40.
N-PSDB; AAH67170.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-DEC-2000; 2000EP-0127688
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                                      Loca1
           159;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 248
                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'n 'n
                                                                                                                                                                Patent Office.
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                                                                                                              378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bacterium;
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; 2000JP-0159162.
; 2000JP-0280988.
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Senoh A, Ikeda
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   synthesis.
                                                                                                              AA;
                              40.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid synthesis; vitamin;
        64;
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da M,
Score 761; DB 22;
Pred. No. 2.1e-68;
4; Mismatches 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          378
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                                          This invention relates to a method for identifying a nucleotide or polypeptide sequence that may be a drug target, or essential for growth or viability of an organism. Polynucleotide sequences AAH51947 - AAH52092 represent DNA encoding proteins AAG81096 - AAG81241, Mycobacterium tuberculosis proteins which are potential drug targets. The DNA and protein sequences are used to illustrate the method of the invention. The method involves providing an unknown nucleotide or polypeptide sequences, and comparing it to a number of sequences along with at least one algorithm capable of analysing a functional relationship between nucleotide and polypeptide sequences. The method is useful for characterising the function of nucleic acids and polypeptides that may be useful as a target for a drug or essential for the growth or viability of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying nucleotide or polypeptide sequence for use as drug target, involves providing algorithm that analyzes a functional relationship between nucleotide or polypeptide sequences, and comparing the
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                  Claim 2;
                                     as vaccine
diagnostic
                                                                           N-PSDB;
                                                                                                       James
                                                                                                                                           22-JUN-2001;
07-SEP-2001;
                                                                                                                                                                      21-JUN-2002;
                                                                                                                                                                                                            WO2003000721-A2
                                                                                                                                                                                                                                                                                                                                    ABP57500 standard;
                                                                                                                         (MICR-)
                                    mycobacterial peptide, its fragment, variant or
vaccine for treating or preventing mycobacterial
gnostic reagents for identifying such infections
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DB; ABZ71126.
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                   Page 235-236; 246pp;
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gene therapy; mycobacterial infection.
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ABP57504 represent mycobacterial

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acid sequences

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RESULT 10
ABP78786
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          Fontana
                                                                                                                                                                 12-FEB-2002;
                                                                                                                                                                                                                     10-OCT-2002
                                                                                                                                                                                                                                                                                                                     Neisseria gonorrhoeae
                                                            (CHIR-)
                                                                                                          12-FEB-2001; 2001GB-0003424
                                                                                                                                                                                                                                                                      W0200279243-A2
                                                                                                                                                                                                                                                                                                                                                                           Antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABP78786 standard; Protein;
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nes 156; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                             gonorrhoeae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       368
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          MR.
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                                                            CHIRON SPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMGEQ 372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VKVGNQVLESLNLRPRSLEIVSCPSCGRAQVDVYTLANEVTAGLDGLDVPLRVAVMGCVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AVESYRLLAKQIDQPLHLGITEAGGARSGAVKSAIGLGLLLSEGIGDTLRVSLAADPVEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KNIPIRIGVNAGSLEKDLQEKYGEPTPQALLESAMRHVDHLDRLNFDQFKVSVKASDVFL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MVAAYELLAARCDYPLHLGVTEAGPAFQGTIKSAVAFGALLSRGIGDTIRVSLSAPPVEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGIPIRIGVNAGSLDKRFMEKYGKATPEALVESALWEASLFEEHGFGDIKISVKHNDPVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AEAFKLIKQQVNVPLVADIHFDYRIALKVAEYGVDCLRINPGNIGN-EERIRMVVDCARD 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NGPGEAREADLGVASGNGKGQIFVRGEVIKTVPEAQIVETL---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADALAEIARHSQIPVVADIHFQPRYIFAAIDAGCAAVRVNPGNIKEFDGRVGEVAKAAGA
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        Pizza M,
                                                                                                                                                              2002WO-IB02069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry
                                                                                                                                                                                                                                                                                                                                                                         infection;
                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,
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     Masignani
                                                                                                                                                                                                                                                                                                                                                                         vaccine;
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Pred. No. 2e-67;
ζ,
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                                                                                                                                                                                                                                                                                                                                                                      gene therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to proteins from Neisseria gonorrhoeae. Also disclosed are the nucleic acid molecules encoding the proteins an antibodies that specifically bind to the proteins. The composition comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing N. gonorrhoeae infection, this may be in the form of a vaccine or gene therapy. Sequences given in records ABP76736-ABP81046 represent nucleic acid molecules of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 200
N-PSDB;
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                                  321
                                                              304
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DB; ABZ39756.
      364
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                                                                                                                                                                                                                                                                                                                           DAAEAFKLIKQQVN-----VPLVADIHED-YRIALKVAEYG--VDCLRINPGNIG----N
                          TGGNKKSGLYEDGVRKDRLDNNDMIDQLEARIR-----AKASQLDEARRIDVQQV 370
                                                           TTSTVFQELAQDVQNYLRQKMSIWRTLYPGVESLNVAVMGCVVNGPGESKLADIGISLPG
                                                                                                                                                SAIGLGLLLSEGIGDTLRVSLAADP----VEEIKVGFDILKSLRIRSRGINFIACPTCSR
                                                                                                                                                                                                         MRHVDHLDRLNFDQFKV--SVKASDVFLAVESYRLLAKQIDQPLHLGITEAGGARSGAVK
                                                                                                                                                                                                                                        DEKFAFMIRTAAENDKAVRIGVNWGSLDQSLAKRMMDANLVSSAPKPPEEVMKEALIVSA
                                                                                                                                                                                                                                                                                                                                                         LQRRKTHQVLIDHITVGSEAPVVIQSMTNTDTADAKATALQIKELSDAGSEMVRITVNSP
TGETPVAPVYVDGERKVTLKGNNIASEFLAIVEEYVKTNYGKNSSKRNKGKVIPIQSL
                                                                                       QEFDVIGTV-----NALEQR-----LEDIITPMDVSIIGCVVNGPGEALVSTLGV----
                                                                                                                     STAALSVLLQEGIGDTIRISLTPEPGSPRTQEVVVGQEILQTMGLRSFTPMVTACPGCGR
                                                                                                                                                                              LESAEKAVLLGLPEDKIILSCKVSAVHDLIQVYRELGSRCVYPLHLGLTEAGMGSKGIVA
                                                                                                                                                                                                                                                                    EERIRMVVDCARDKNIPIRIGVNAGSLEKDLQEKY------GEPTP-----QALLESA 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from Neisseria gonorrheae, useful for the manufacture for treating or preventing N. gonorrheae infection - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   421 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 487;
                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      28.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                        87;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 534; DB 24;
Pred. No. 3.1e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  English.
                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      142;
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RESULT 11
AAY37164
W09928475-A2
                                        Chlamydia trachomatis
                                                             bartholinitis;
                                                                                 paratrachoma;
                                                                                           Vaccine; eye disease;
                                                                                                              Amino acid sequence of a Chlamydia trachomatis protein
                                                                                                                                      07-OCT-1999
                                                                                                                                                                               AAY37164
                                                                        nongonococcal
                                                                                                                                                                              standard;
                                                                                                                                      (first
                                                                       uretritis;
                                                                     inclusion conjunctivitis; genital disease; peri uretritis; epidymitis; cervicitis; salpingitis;
                                                        uretritis; epidymitis; pneumopathy; venereal
                                                                                                                                                                             Protein;
                                                                                                                                    entry)
                                                                                          conventional trachoma;
                                                                                                                                                                              611
                                                                                                                                                                              Å
                                                          lymphogranulomatosis
                                                                                          nonendemic trachoma;
                                                                              perihepatitis;
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10-JUN-1999

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28-NOV-1997;
17-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome sequence of Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY36754-Y37949 are encoded by open reading frames (ORFS) of the genome of Chlamydia trachomatis (see AAZ01425). The polypeptides can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye diseases such as conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion conjunctivitis; genital diseases such as perihepatitis, bartholinitis; pneumopathy in breast feeding infants; penithepatitis, bartholinitis; pneumopathy in breast feeding infants; and veneraal lymphogranulomatosis. The polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 943-944; 1755pp; English.
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                                                                                                                                                                                                                                                                                                                                                  VHACEHIKDRLIQQNISIPLVADIHFFPQAAIHVVDC-VDKVRINPGNYVDKRNMFTGKI 138
                                                                                                                                                                                                                                                                                                                                                                        AEAF-----KLIKQQVNVPLVADIHFDYRIALKVAEYGYDCLRINPGN------I
                                                                                                                                                                                                                                                                                                       YSDEQYAHSLEHLMNKFSPLYEKCKRLGKAMRIGVNHGSLSERVTQRYGN-TIEGMVYSA
                                                                                                                                                                                                                                                                                                                          GNEERIRMVVDCARDKNIPI------RIGVNAGSLEKDLQEKYGEPTPQALLESA 161
GEALVSTLGVTGGNKKSGLYE
                               GFLILQSANIRSVTVEYVSCPGCGRTLFDLLAVSQRIRERTKHLPGGLKIAVMGCIVNGP
                                                     GFDILKSLRIRSRGINFIACPTCSRQEFDVIGTVNALEQRLEDIITPMDVSIIGCVVNGP
                                                                            FFSLRQHSTQPVCLSFSLDPHLSKNEAIIDLSARLGALLLDGLGSCVLLDFVDIKLSRTL
                                                                                                                      VPKAMRSSPIVSEIEKHLLVFNKEDAPILNPMNEEEWLSEETLSAPFVYFEVTDIHTARR
                                                                                                                                                                   SKQLGTRNTLNTPPWDNVYGLLINLTDVQLLTAEPIELLQCLGIDTTTGKIDPTTPEGVV
                                                                                                                                                                                                               IVKSAVGIGTLLSEGLGDTIRCSLTGSPINEIPICIDLLKQTTELSERWGEADNPFAIHS
                                                                                                                                                                                                                                    AVKSAIGLGLLLSEGIGDTLRVSLAADPVEEIKV-----
                                                                                                                                                                                                                                                          LEYAEVCVAMDYHDVIFSMKSSNPKVMVAAYRSLAYELDQREWSYPLHLGVTEAGSGTAG
                                                                                                                                                                                                                                                                                 MRHVDHLDRLNFDQFKVSVKASDVFLAVESYRLLAKQIDQ-----PLHLGITEAGGARSG
                                                                                                                                                                                                                                                                                                                                                                                              RRKTLPVRIGDLFVGSEHSIKIQSMTTTATTDVDGTVRQICALQELGCDIVRVTVQGLRE
                                                                                                                                                                                                                                                                                                                                                                                                                  RRKSTRIYVGNVPIGDGAPIAVQSMTNTRTTDVEATVNQIKALERVGADIVRVSVPTMDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use in treating these diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      611 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0107077.
97FR-0015041.
97FR-0016034.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     26.3%;
23.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                          76;
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     490; DB 20;
No. 1.7e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                           109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                611;
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AAY34971
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δõ
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Best Local S
Matches 111
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21-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY34971;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Griffais
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9927105-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-357842/30
                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GEST ) GENSET
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  216
                       198
                                            161
                                                                   139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                558 GEMADADFGYVG--SKPGMID 576
                                                                                                                                                                                                       111;
                                                                                                              80
                                                                                                                                     69
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                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                  621 AA;
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disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used immunogenic compositions as vaccines. Vectors containing C. pneumonia nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY34971 standard; Protein; 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome sequence of Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vaccine; neutralising epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY34584-Y35879 represent the proteins encoded by all the open reading frames in the complete genome (see AAX91990) of Chlamydia pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         epitope of C. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neumoniae causes respiratory disease such as pneumonia and pronchitis and is thought to be a contributing factor in heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         885-886; Disclosure;
GAVKSAIGLGLLLSEGIGDTLRVSLAADPVEEIKVGFDILKSLRI
                                                                                                                                                                                                                                                                            AQACEKIKERLIALGLNIPLVADIHFFPQAAMLVADF-ADKVRINPGNYIDKRNMFKGTK 138
                                                                                                                                                                                                                                                                                                                                              RRKTHTVRIGNLYIGSDHSIKTQSMTTTLTTDIDSTVEQIYALAEHNCDIVRVTVQGIKE
                                                                                                                                                                                                                                                                                                                                                                                            RRKSTRIYVGNVPIGDGAPIAVQSMTNTRTTDVEATVNQIKALERVGADIVRVSVPTMDA
                                             AIEYIAVCEKLNYRDVVFSMKSSNPKIMVTAYRQLAKDLDARGWLYPLHLGVTEAGMGVD
                                                                                           AMRHVDHLDRLNFDQFKVSVKASDVFLAVESYRLLAKQID-----QPLHLGITEAGGARS
                                                                                                                                       IYTEASYAQSLLRLEEKFAPLVEKCKRLGKAMRIGVNHGSLSERIMQKYGD-TIEGMVAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence of a
                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0107078.
97FR-0014673.
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                                                                                                                                                                                          IGNEERIRMYVDCARDKNIPIRIGVNAGSLEKDLQEKYGEPTPQALLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1912pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                               55;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 470.5; |
Pred. No. 1.7e
55; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.7e-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 84;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  621;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           an be used in pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                    160
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                                                                                                                                                                                            of methyl-D-crythritol phosphate (MEP) pathway) that encodes rice, Arabidopsis thaliana or Escherichia coll GCPE protein gcpE is useful for producing a transgenic plant such as Brassica campestris, B. napus, canola, castor bean, coconut, cotton, crambe, linseed, maize, mustard, oil palm, peanut, rapeseed, rice, safflower, sesame, soybean, sunflower, or wheat with an increased isoprenoid (tocopherol) compound level. The expression of GCPE protein in organisms increases the level of tocopherol substrate such as isopentyl diphosphate and dimethylallyl diphosphate biosynthesis. Transgenic organisms overexpressing GCPE protein can nutritionally enhance food and feed sources. Overexpression
                                          the same species, and to obtain nucleic acid homologues. gcpE is also used as or primers. The recombinant vectors are used in plant transformation or transfection. gcpE an also act as markers capable of detecting polymorphisms such as single nucleotide polymorphisms (SNPs). gcpE is also used to determine the level or pattern of expression of the protein. The present sequence is Arabidopsis thaliana GCPE protein.
                                                                                                                                         of GCPE protein in transgenic plant may provide tolerance to stresses e.g., oxidative stress tolerance such as to oxygen or ozone, UV tolerance, etc. gcpE may be used to obtain nucleic acid molecules from
                                                                                                                                                                                                                                                                                                                                                                                                                                gcpE nucleic acid which is an essential gene of the methyl-D-erythritol
phosphate pathway, encoding a fully defined GCPE protein which is
useful for increasing levels of tocopherol substrates in plants -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI;
Sequence
                                                                                                                                                                                                                                                                                                                                                                        The invention relates
                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 140-142; 155pp; English
                               gcpE gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Boronat A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-AUG-2000; 2000US-223483F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-AUG-2001; 2001WO-US24335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Valentin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oxidative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  food;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE19650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE19650 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MONS ) MONSANTO TECHNOLOGY LLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2002-227151/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene; methyl-D-erythritol phosphate; MEP; dimethylallyl dipl
genic plant; isoprenoid compound; tocopherol; isopentyl dipl
feed source; transfection; single nucleotide polymorphism;
tive_stress tolerance; UV tolerance; transformation; chromo:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Campos N, F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                thaliana GCPE protein
                               The present sequence is located on chromosome V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers 32..33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Plastidial targeting peptide cleavage site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein;
                                                                                                                                                                                                                                                                                                                                                                      to gcpE nucleic acid molecule,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rodriguez-concepcion M, h TV, Venkatramesh M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    740
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seeman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diphosphate;
diphosphate;
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gene

Query Match

24

.88;

Score 462;

DВ 23;

Length 740;

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humans or al activity

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RESULT 14
AAB45693
ID AAB45
XX AAB45
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IN 15-MA
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                   This invention describes a novel method for incorporating gcpE and yfgB genes into viruses and cells for increasing isoprenoid content and identifying e.g. antimicrobial agents, comprises using DNA sequences (I) from the gcpE or yfgB genes of bacteria or parasites or DNA sequences (II) which hybridize to the specified genes or encode a plastid protein with the same biological activity as those encoded by the genes. The invention also describes (I) plant cells containing (I) or (II); (2) transformed plant cells, and transgenic plants regenerated from them, that contain (I) or (II); (3) determining the enzymatic activity of a gcpE protein; or (4) screening compounds (A) that have antimycotic, antiparasitic or antiviral activity in humans or animals or antiviral.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Incorporating gcpE and yfgB genes into viruses and cells, for increasing isoprenoid content and identifying e.g. antimicrobial agents, comprises using DNA sequences from bacteria or parasites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-MAY-1999;
21-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 21-23; 36pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAC82654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-025196/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jomaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antimycotic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P. falciparum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (JOMA/) JOMAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARDK----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antiparasitic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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99DE-1023568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         yfgB; antimicrobial; parasitic; antiviral;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----NIPIRIGVNAGSLEKDLQEKYGEPTPQALLESA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transgenic plant; agri
fungicidal; herbicidal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   agriculture;
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(ii) for d
and (iii)
potential
                                                                                                                                                                                                                                   1-deoxy-D-xylulose-5-phosphate reductoisomerase; isoprenoid biosynth deoxy-D-xylulose-phosphate; 1-deoxy-D-xylulose-5-phosphate synthase; gcpE; antimycotic; antibictic; antiviral; antiparasitic; antimicrobi bactericide; fungicide; herbicide; treatment; disease.
                                                                                                                                                                                                                      Plasmodium falciparum.
                                                                                                                                                                                                                                                                                     P. falciparum
                                                                                                                                                                                                                                                                                                        07-JUL-2000
                                                                                                                                                                                                                                                                                                                                            AAW90883 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for
         Claim
                         New nucleic acid, useful Cherapeutically and to screen for antimicrobials and herbioldes, encode proteins involved in biosynthesis by the deoxyop-xylulose-phosphate route -
                                                                N-PSDB;
                                                                                             Jomaa
                                                                                                               (JOMA/) JOMAA
                                                                                                                                 22-SEP-1998;
21-MAY-1999;
                                                                                                                                                             22-SEP-1999;
                                                                                                                                                                                30-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        herbicidal agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     used: (i) to increase the isoprenoid levels in viruses and cells; ) for determining the enzymatic activity of gcpE and yfgB proteins; (iii) to identify compounds that inhibit activity of gcpE, i.e. ential antibacterial, antimycotic, antiparasitic or antiviral agents use in humans or animals, or antiviral, antiparasitic, fungicidal herbicidal agents for agriculture.
                                                                                                                                                                                                                                                                                                                                                                                                                              294
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                                                                                                                                                                                                                                                                                                                                                                                                                       AAX82996.
                                                                                                                                                                                                                                                                                                                                                                                        KRLPTREVVIGNVKIO
        Page 41-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       679 AA;
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                                                                                                                                                                                                                                                                                    gcpE
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98DE-1043279.
99DE-1023567.
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      44 pp
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38.98;
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          German.
                                                                                                                                                                                                                                                                                                                                            752 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 460; DB 22;
Pred. No. 2.3e-37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 679;
                                                                                                                                                                                                                                                                   isoprenoid biosynthesis;
                                                                                                                                                                                                                                                  antimicrobial;
                                   e.g.
isoprenoid
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                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes novel polypeptides and their analogs which are involved in isoprenoid biosynthesis by the deoxy-D-xylulose-phosphate route. The proteins described include 1-deoxy-D-xylulose-5-phosphate reductoisomerase, 1-deoxy-D-xylulose-5-phosphate synthase and the gcpE protein. The products of the invention have antimycotic, antibiotic, antiviral, antiparasitic, antimicrobial, bactericide, fungicide and herbicide activity. The encoding nucleic acid sequences of the invention are used for prevention or treatment of diseases in humans and animals are used for prevention or treatment of diseases in humans and animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antimicrobials, antiparasitic agents, antivirals, fungicides, bactericides and herbicides, for use in human or veterinary medicine or agriculture). This sequence represents the Plasmodium falciparum gcpE protein described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          are used for prevention or treatment of diseases in humans and and also to screen compounds enzyme inhibitory activity (potential
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                  RRKSTR-IYVGNVPIGDGAPIAVQSMTNTRTTDVEATVNQIKALERVGADIVRVSVPTMD 67
DNGRIKSYLGIGSLLYDGIGDTIRISLTEDPWEELTPCKKLVENLKKR
                    RSGAVKSAIGLGLLLSEGIGDTLRVSLAADPVEEIKVGFDILKSLRIR
                                                                                                                                          VYKTKEEFDEGKLFIKEKFVPLIEKCKR-LNRAIRIGTNHGSLSSRVLSYYGD-TPLGMV
                                                                                                                                                                                                                EAQASYHIKEKLLSENVNIPLVADIHFNPKIALMAADV-FEKIRVNPGNYVDGRKKWIDK
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                                                                                                                                                                                                                                                                                                                                                             56;
                                                                                                                                                                                                                                                                                                                                                                              Score 446; DB 21;
Pred. No. 7.1e-36;
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Search completed: August 12, 2003, 09:56:03 Job time: 88 secs

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/cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
/cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
/cgn2_6/ptodata/1/1aa/B_COMB.pep:*
/cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
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              US-09-066-046-6
US-09-252-991A-30838
US-08-975-762-50
US-09-252-991A-29387
US-09-106-582-50
US-09-129-964-2
US-09-128-352-7730
US-09-328-352-7730
US-09-328-352-7730
US-09-328-352-7736
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US-09-328-352-7906
US-09-198-452A-389
US-09-252-991A-29105
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4730, Appl
7436, Ap
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US-08-827-190-6
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                                                                                             Query Match
Best Local Similarity
                                                                            Matches
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                                                                                                                                                                                                                                                           TELEFAX: (415) 397-8338 INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Rather
                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: CA
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAITOLI, Peter G.
NAME: CAITOLI, Peter G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/827,190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                   MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: METITLE OF INVENTION: Ut NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                    STRANDEDNESS:
TOPOLOGY: 111
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                                                                                                                                                                                                                                                                                                                  TELEPHONE:
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                                                                                                                                                                                                                                          LENGTH:
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                   1 MHNQAPIQRRKSTRIYVGNVPIGDGAPIAVQSMTNTRTTDVEATV--NQIKALERVGADI 58
                                                                                                                                                                                                                         amino acid
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MHNQAPIQRRKSTRIYVGNVPIGDGAPIAVQSMTNTRTTDVEATVFTNQIKALERVGADI 60
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                                                                            Conservative
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                                                                                         96.5%;
96.9%;
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                                                                                                                                                                                                                                                                                                                                                        CASE-02443
                                                                        Score 1800; DB 2;
Pred. No. 4.9e-188;
D; Mismatches 0;
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US-09-170-187-6
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APPLICANT: Rather, Phil
TITLE OF INVENTION: Met.
TITLE OF INVENTION: Ut.
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                 Query Match
Best Local Sim
Matches 372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/09170187 Patent No. 6383745
                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: CASE-02443
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 384 amino acid
                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION: NAME: Carroll, Peter G
                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                        NAME: Carroll, Peter G. REGISTRATION NUMBER: 32,837
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/170,187 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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1 MHNQAPIQRRKSTRIYVGNVPIGDGAPIAVQSMTNTRTTDVEATV--NQIKALERVGADI 58
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T: 220 Montgomery Street, Su
San Francisco
California
                                                       Similarity
                                                                                                                                                                              amino acid
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                                     Conservative
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                                                                                                                        peptide
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Methods For Screening For Antimicrobials
Utilizing aarC And Compositions Thereof
                                                     96.5%;
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                                     0;
                                   Score 1800; DB 4;
Pred. No. 4.9e-188;
0; Mismatches 0;
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                                                                    Length 384;
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Query Ma Best Loo Matches	RESULT 3 US-08-827-190-5 Sequence 5, E Patent No. 58 GENERAL INF APPLICANT TITLE OF 1 TITLE OF 1 TITLE OF 1 TITLE OF 2 TOTATE: COUNTRY ZIP: 94 COMPUTER I MEDIUM 1 COMPUTER I MEDIUM 1 COMPUTER I COMPUTER I MEDIUM 1 COMPUTER I COMPUTER I COMPUTER I MEDIUM 1 COMPUTER I CO	Db	Qy	Db	Qy	Db V	ָרָי בְּי	Qy St	Db	Qy	Qу Db	Db
Match 87.0%; Score 1622.5; DB 2; Length 365; Local Similarity 88.4%; Pred. No. 1.2e-168; es 320; Conservative 24; Mismatches 17; Indels 1; Gaps 1;	HIT 3 18-827-190-5 Iquence 5, Application US/08827190 tent No. 588367 EPPLICANT: Rather, Philip N. ITILE OF INVENTION: Methods For Screening For Antimicrobials TITLE OF INVENTION: Willzing aarC And Compositions Thereof NUMBER OF SEQUENCES: 13 CORRESPONDENCE ADDRESS: ADDRESSEE: Medien & Carroll, LLP STREET: 220 Montgomery Street, Suite 2200 CITY: San Francisco COUNTRY: United States of America ITI: 94104 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM C compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTWARE: DATENTION Release #1.0, Version #1.30 CURRENT APPLICATION NAMA: SOTWARE: PATENTION: 435 ATTORNEY/AGENT INFORMATION: NAME: CARTOLL, Peter G. REGISTRATION NUMBER: US/08/827,190 FILING DATE: TELEPHONE: (415) 705-8410 TELEPAX: (415) 39-8338 INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 365 amino acids TYPE: amino acids TYPE: amino acids TYPE: amino acids TYPE: protein MOLECULE TYPE: protein NB-827-190-5	361 EARTRAKASQLDEARRIDVQQVEK 384	349 EARIRAKASQLDEARRIDVQQVEK 372	301 LEDIITPMDYSIIGCVVNGPGEALVSTLGVTGGNKKSGLYEDGVRKDRLDFTNNDMIDQL 360	291 LEDITTPMDVSIIGCVVNGPGEALVSTLGVTGGNKKSGLYEDGVRKDRLDNNDMIDQL 348	233 GDILKYSLANDEYFELKYGFDILKSLKIRSKGINFIACPTCSRQEFDVIFTGTVNALEQR 300	QENVSVANASUVE HAVESI KHIMANQIDQE URBUSI BANGGANSON KURII KURULIKETER. QENVANASUVE HAVESI KURANQIDQI KARANDI KORILIKETER. TRSRQINFIACIDTCSROEFDVIGTVNALEOR	175 QFKVSVKASDVFLAVESYRLLAKQIDQPLHLGITEAGGARSGAVKSAIGLGLLLSEGI 232	121 RIRMVVDCARDKNIPIRIGVNAGSLEKDLQEKYGEPTPQALLESAMRFTHVDHLDRLNFD 180	117 RIRMYVDCARDKNIÞIRIGVNAGSLEKDLQEKYGEPTPQALLESAMRHVDHLDRLNFD 174	59 VRVSVPTMDAAEAFKLIKQQVNVPLVADIHFDYRIALKVAEYGVDCLRINPGNIGNEE 116 	

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; MOLECULE TYPE: US-09-170-187-5
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US-09-170-187-5
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                                                       TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENCTH: 365 amino acids
TYPE: amino acid
TOPOLOGY: linear
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/09170187 Patent No. 6383745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                              REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: CA.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
                                                                                                                                                                         ATTORNEY/AGENT INFORMATION: NAME: Carroll, Peter G.
                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                      CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll,
                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
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                                                                                                                                                               REGISTRATION NUMBER:
                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                              SOFTWARE:
                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: San Francisco
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Methods For Screening For Anthony

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 Score 1622.5; DB 4; Pred. No. 1.2e-168;
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US-09-252-991A-22991
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US-09-252-991A-22991
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PRIOR FILLING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 22991
LENGTH: 547
TYPE: PRT
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Best Local
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Patent No. 6551795
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SIIGCVYNGPGEALVSTLGVTGGNKKSGLYEDGVR-KDRLDNNDMIDQLEARIRAKASQL
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GENERAL INFORMATION:
APPLICANT: MAIC J. Rubenfield et al.
APPLICANT: MAIC J. Rubenfield et al.
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
FILE REFERENCE: 107196.136 CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18 UMBER: US 60/074,788 1998-02-18 73.6%; Score 1372.5; DB 4 73.8%; Pred. No. 4.9e-141; DB 4; Length 547;

48;

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Gaps

238 60

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Sequence 389, Application US/09198452A
Patent No. 6559294
GENERAL INFORMATION:
APPLICANT: Griffais, R.
TITLE OF INVENTION: Chlamydia pneumoniae
TITLE OF INVENTION: thereof and uses th
TITLE OF INVENTION: and treatment of in
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US-09-328-352-7906
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US-09-328-352-7906
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US-09-198-452A-389
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SEQ ID NO 7906
LENGTH: 378
TYPE: PRT
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TITLE OF INVENTION: NUCLEIC ECID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANIO FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06604
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US-09-198-452A-389
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US-09-252-991A-29105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 22105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 29105, Application Patent No. 6551795
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LENGTH: 621
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Best Local
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CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 198-11-24
NUMBER OF SEQ ID NOS: 6849
                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788
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                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Pseudomonas aeruginosa
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                                                                                                                               LVEVENTVRIIKQSAAAVGKELKVAPLHSASRIYERAEMQFEQGKTDHPYDYACLLDV--
                                                                                                                                                                                                                        PVRKADSGNEYRVNAPTGSGKSVAMVMMA
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Pred. No. 2.5e-42;
                                                                                                                                                                                                                                                                                                                Score 112.5; DB 4;
Pred. No. 0.0084;
0; Mismatches 140;
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                                                                                     -- IGNEERIRMVVDC
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US-09-066-046-6
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US-09-066-046-6
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GENERAL INFORMATION:
APPLICANT: MURPHY, Cheryl STOREY, James
                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION MIMBER: US/09/066,046A
FILING DATE: 24-Apr-1998
CLASSIFICATION: <UDKnown>
ATTORNEY/AGENT INFORMATION:
ATTORNEY CONTENT OF THE PARTICLE TO THE PARTICL
                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: DNA (90 HYPOTHETICAL: NO ANTI-SENSE: NO
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 578 amino acids
                                                                                                                                                                                            SEQUENCE DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION
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CORRESPONDENCE ADDRESS:
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COUGHLIN, Richard T.
COUGHLIN, RICHARD TERTIATION OF GRANULOCYTIC
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                                                                    88;
          7 IQRRKSTRIYVGNVP-----IGDGA-----PIAVQSMTNTRT-TDVEATVNQ-
                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
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REFERENCE/DOCKET NUMBER: 10
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STREET: 60 State Street
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STATE: MA
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Pred. No. 0.
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SEQ ID NO 30838
LENGTH: 980
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS CURRENT APPLICATION NUMBER: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR ETILING DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
          592
                                                       175
                                                                                                        540
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                                                                                                                                                  125 ARDKNIPIRIGVNAGSLEKDLQEKYGEPT---PQALLES---
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                                                                                                                                                                                                                                                                                                                                            16 YVGNVPIGDGAPIAVQSMTNTRTTDVEATVNQIKALERVGADIVRVSVPTMDAAEAFKLI 75
                                                                                                                                                                                                                                                                                                                                                                                                           88;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                              TAQAQLPI-----LATVLAEVLGEPAFVQPRVDAEGFAAADLVLLPVVAEGQYMAFG
                                                                                                                                                                                                                                              KQQVNVPLVADIHF-----DYRI-----ALKVAEYGVDCLRINPGNIGNEERIRMVVDC
                                                                                                                                                                                                                                                                                                FVDVVRLPPGAPRSRTRIVADQVVDVGT-----EGIHRPVPPAMRTAQPDLQAARSLGV-
QGQVVLPGQAVATGIEA-----RVETAILIGIGLVLAAPGLEGHQPGIERSEAGTA-AD
                                                 QFKVSVKASDVFLAVESYRLLAKQIDQPLHLGI-----
                                                                                                                                                                                                 --QVGIAVVGVVEFVEGRRLECRAVVDGEAQRVAQ-----RVAPGGAAGVVHAELLVVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GDLKSEVSVEADAGMQQEAGISDQETQATEEVEKVEVSVEADAGMQQEL--VDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VSVEADAGMQQEAGISD--QETQATEEVEKVEVSVETKTEEPEVILEEGTLIDLEQPVAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IKALERYGADIYRYSYPTMDAAEAFKLIKQQYNYPLYADIHFDYRIALKYAEYGYDCLRI 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GNKKSGL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QKEVISGQQEQEIAEALEGTEAPVEVKEETEVLLKEDTLIDLEQPVAQVPVVAEAELPGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EAAEAIVPSLEENKLQEVVVAPEAQQLESAPEVSAPAQPESTVLGVTE-----GDLKSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------KASDVFLAVESYRL-LAKQIDQPLH-----LGITEAGGARSGAVKSA 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QALLESAMRHYDHLDRLNFDQFKVSV------------
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                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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20.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Score 106.5; DB Pred. No. 0.033;
                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                 ----TEAGGARSG
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QY 83 LVADIHFDYRIALKV95-AEYGVDCLRINPGNIGNEERIRMVVDCARDKNIPIRIGVNAG 139	172 APAIEEVETEEQEVIÜEEGTLIDLEQPVAQVPVVAEAELPGVEAAEAIVPSLEENKLQEV	QY 48 IKALERVGADBIVRVSVPTMDAAEAFKLIKQQVNVP-82	QY 7 IQRRKSTRIYYGNVP=GIGDGA	5.7%; score 105.5; DB 3; Length 578; Similarity 19.5%; Pred. No. 0.018; Pred. No. 0.018; Conservative 77; Mismatches 176; Indels 123; Gaps	PE	; LENCTH: 578 amino acids ; TYPE: amino acid ; STRANDEDNESS: ; TOPOLOGY: linear	; TELEPHONE: 206-622-4900; ; TELEPAX: 206-682-6031 ; INFORMATION FOR SEO ID NO: 50: ; SEQUENCE CHARACTERISTICS:	; NAME: Maki, David J.; REGISTRATION NUMBER: 30,392; REFERENCE/DOCKET NUMBERS 210121.439; TELECOMMUNICATION INFORMATION:	APPLICATION NUMBER: US/08/975,762 FILING DATE: 21-MAR-1997 CLASSIFICATION: 424 ATTORNEY/AGENT INFORMATION:	OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:	COMPUTER: IBM PC compactible	CITY: SEATTLE STATE: Washington COUNTRY: USA TID. 00104	SSS	les, ight ion	RMATION:	WESOLF 11 US-08-975-762-50 ; Sequence 50, Application US/08975762 ; Patent No. 6207169	i	Oy 308 (QYEN 3/2	753 LGALAV	Qy 327 SGLYEDGYRKDRLDNNDMIDQLEARIRAKASQLDEARRIDV 367	694 VAVAVSVWLIARSTGAEGIDPRRIE-AAHPEAVPAVAGAAADPGAALQGLWGAVTGGEER	277 EFDVIGTVNALEQRLEDIITPMDVSIIGCVVNGPGEALVSTLG-VTGGNKK		ON 217 AVKGATGLGIJI.SEGIGDMI.RVSIJAADPVBEIKVGEDIIKSLRIRSRGINEIACPTCSRO 276
מוואל הינוח אחר אינוי הינו הינו הינו הינו הינו הינו הינו	Qy 225 GLLLSEGIGDTLRVSLAADPVEEIKVGFDILKSLRIRSRGINFIACPTCSRQ 276 : : : : :	Db 345 PSLEENKLQEVVVAPEAQQLESAPEVSAPAQPESTVLGVTEGDLKSEVSVEADA 398	KASDVFLAVESYRL-LAKQIDQPLHLGITEAGGARSGAVKSAIGL	140 SLEKDLQEKY-GEPTPQALLESAMRHVDHLDRLNEDQFKVSV	83	Qy 48 IKALERYGADIVRVSVPTMDAAEAFKLIKQQVNVP 82	Oy 7 IQRRKSTRIYVGNVPIGDGAPIAVQSMTNTRT-TDVEATVNQ- 47	Query Match 5.7%; Score 105.5; DB 3; Length 578; Best Local Similarity 19.5%; Pred. No. 0.018; Matches 91; Conservative 77; Mismatches 176; Indels 123; Gaps 21;	; LENGTH: 578 ; TYPE; PRT ; ORGANISM: Ehrlichia sp. US-09-295-028-50	; NUMBER OF SEQ ID NOS: 85 ; SOFTWARE: FastSEQ for Windows Version 3.0 ; SEQ ID NO 50	REFERENCE: 2101 NT APPLICATION NT FILING DATE:	zz	; GENEKAL INFORMATION: ; APPLICANT: Reed, Steven G. ; APPLICANT: Lodes, Michael J. · APPLICANT: Houghton, Raymond L.	ن آڻ اِ	מסמנו יי וויסממ	QY 330YEDGYRKDRLDNNDMIDQLEARIRAKASQLDEARRIDV 367 : ::: : : :	457	277	Qy 225 GLILSEGIGDTLRVSLAADPVEEKKVGFDILKSLRIRSRGINFIACPTCSKQ 2/6	VLGVTEGDLKSEVSVEADA	OY 181KASDVFLAVESYRL-LAKQIDQPLHLGITEAGGARSGAVKSAIGL 224	285	140	Db 232 VVAPEAQQLESAPEVSAPAQPESTVLGVAEGDLKSEVSVEANADVAQKEVISG 284

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US-09-106-582-50
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APPLICANT: Reed, S
APPLICANT: Lodes, I
APPLICANT: Houghton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 50,
Patent No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:

NAME: Mak1, David J.

REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 2101

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Houghton, Raymond
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: . 578 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 29-JUN CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Seattle
STATE: Washing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ocal
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                                                                                                                                                                                                                                                                      172
                                                                                                                                                                                                                                                                                                                                                      112 VQEEEGTGMYLINAPEKAVVRFFKIEKSAAEEPQTVDPSVVESATGSGVDTQEEQEIDQE
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                                                                                                                                                                                                                                                                                                                                                                                                  7 IQRRKSTRIYVGNVP------IGDGA------PIAVQSMTNTRT-TDVEATVNQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                      QQEQEIAEALEGTEAPVEVKEETEVLLKEDTLIDLEQPVAQVPVVAEAELPGVEAAEAIV 344
                                                                                                       SLEKDLQEKY-GEPTPQALLE--SAMRHVDHLDRLNFDQFKVSV-----
                                                                                                                                                                                                     LVADIHFDYRIALKV---AEYGVDCLRINPGNIGNEERIRMVVDCARDKNIPIRIGVNAG 139
                                                                                                                                                                                                                                                      APAIEEVETEEQEVILEEGTLIDLEQPVAQVPVVAEAELPGVEAAEAIVPSLEENKLQEV
                                                                                                                                                                                                                                                                                                     IKALERVGAD-----KLIKQQVNVP
          -----KASDVFLAVESYRL-LAKQIDQPLH-----LGITEAGGARSGAVKSAIGL----
                                                                                                                                                      VVAPEAQQLESAPEVSAPAQPESTVLGVAEGDLKSEVSVEANADVAQKE-----VISG 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6306402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELPGVEAAEAIVPSLEENKLQEVVVAPEAQQLESAPEVSAPVQPESTVLGVTEGDLKSEV 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EFDVIGTVNAL----EQRLEDIITPMDVSIIGCV--VNGPGEALVSTLGVTGGNKKSGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: SEED and BERRY LLP 6300 Columbia Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US/09/106,582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 105.5;
Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .5; DB 4;
0.018;
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RESULT 15
US-09-612-964-2
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29387
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US-09-252-991A-29387
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Best Local
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PATENT NO. 6551795
GEMERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: AUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AUCUEIC ACID AND AMINO ACID SEQUENCES RELATING
FILE REFERENCE: 107196.136
FILE REFERENCE: 107196.136
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SEQ ID NO 29387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR PILING DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 P
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                                                                                                                                                                                                                                    IRSRGINFIACPTCSRQEEDVIGTVNALEQRLEDIITPMDVSIIGCVVNGPGEA-----
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                                                                                                                                                                                     -----FYDMPGRAAVEHDV------DIVLLEQEDFLGTMLGGFGEAHHVEQL 365
                                                                                                                                                                                                                                                                                          VQLAEVGVAAHQLGTLGFGVGGGLGSVLHPEGHGAGARAVLEGE:
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21.8%;
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Pred. No. 0.038;
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NUMBER OF SEQ ID NOS: 12
SEQ ID NO 2
LENGTH: 523
TYPE: PRT
ORGANISM: Escherichia coli
US-09-612-964-2
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Search completed: August 12, 2003, 09:59:12
Job time : 32 secs
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APPLICANT: KOZÍOV YURY IVANÖVÍCH
APPLICANT: VOTOSÁILOVA ELVÍĞA BORÍSOVNA
APPLICANT: VOTOSÁILOVA ELVÍĞA BORÍSOVNA
TITLE OF INVENTION: L'LEUCINE-PRODUCING MICROORGANISM AND METHOD FOR PRODUCING
TITLE OF INVENTION: L'LEUCINE
TITLE OF INVENTION: L'LEUCINE
FILE REFERENCE: 193845USO
CURRENT ETLING DATE: 2000-00-10
PRIOR APPLICATION NUMBER: RÜ 99114325
PRIOR APPLICATION NUMBER: RÜ 99114325
PRIOR FILING DATE: 1999-07-09
NUMBER: CONTROL STANDON NUMBER: RÜ 99114325
PRIOR FILING DATE: 1999-07-09
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Best Local Similarity
Matches 83; Conserv
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                                                                          294 AHSSGIHQDGVLKNREWYEIMTPESIGLNQIQLNLTSRSGRAAVKHRMD 342
                                                                                                                                                                                    265 INFIACPTCSRQEFDV GTVNALE-QRLEDIITPMDVSIIGCVVNGPGEALVSTLGVTGG 323
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Maximum DB seq
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Perfect score:
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length: 2000000000
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Match
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1866
1 MHNQAPIQRRKSTRIYVGNV......RAKASQLDEARRIDVQQVEK 372
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Maximum Match 100%
Listing first 45 summaries
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              Published_Applications_AA: *
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  9 US-09-159-469-50

9 US-09-798-042-50

9 US-09-815-242-12389

9 US-09-815-242-12389

15 US-10-156-761-8947

9 US-09-815-242-10969

15 US-10-260-877-70

9 US-09-815-242-5590

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US-09-881-752A-196

US-10-156-761-9186

US-09-738-626-5705

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US-10-156-761-10088
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Sequence 196, App
Sequence 9186, Ap
Sequence 5705, App
Sequence 256, App
Sequence 50, Appl
Sequence 50, Appl
Sequence 5035, Ap
Sequence 12389, A
Sequence 12389, A
Sequence 10969, A
Sequence 70, Appl
Sequence 10969, A
Sequence 5590, App
Sequence 5590, Appl
                                                                                                                                                                                          Sequence 10098, A Sequence 196, App Sequence 9186, App Sequence 5705, App Sequence 256, App
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Sequence 4379, Ap	10 US-09-738-626-4379		4.7	88.5	45
Sequence 54, Appl	9 US-09-905-983-54		4.8	89	44
Sequence 5, Appli	15 US-10-028-392-5		4.8	89	3
Sequence 5114, Ap	9 US-09-815-242-5114		4.8	89	42
Sequence 5880, Ap	10 US-09-738-626-5880		4.8	89	41
Sequence 11037, A	9 US-09-815-242-11037		4.8	89.5	40
Sequence 8084, Ap	15 US-10-128-714-8084	722	. 8	89.5	39
	15 US-10-156-761-9172		4.8	90	38
Sequence 4, Appli	9 US-09-784-508-4		4.8	90	37
Sequence 71, Appl	10 US-09-971-536-71		4.8	90	36
Sequence 11950, A	9 US-09-815-242-11950		4.8	90.5	ω
Sequence 13475, A	15 US-10-156-761-13475		4.8	90.5	34
Sequence 12534, A	15 US-10-156-761-12534		4.8	90.5	ω ω
Sequence 11826, A	9 US-09-815-242-11826		4.8	90.5	32
Sequence 12128, A	9 US-09-815-242-12128		4.8	90.5	Lul
Sequence 5420, Ap	9 US-09-815-242-5420		4.8	90.5	30
Sequence 9, Appli	10 US-09-938-275-9		4.9	91	29
Sequence 14612, A	15 US-10-156-761-14612		4.9	91	28
Sequence 667, App	15 US-10-102-806-667		4.9	91	27
Sequence 6091, Ap	10 US-09-738-626-6091		4.9	91.5	26
Sequence 13072, A	9 US-09-815-242-13072		4.9	91.5	25
Sequence 13258, A	9 US-09-815-242-13258		4.9	91.5	24
Sequence 8, Appli	10 US-09-845-583-8		4.9	92	23
Sequence 5600, Ap	10 US-09-738-626-5600		4.9	92	22
Sequence 11266, A	9 US-09-815-242-11266		4.9	92	21
Sequence 4018, Ap	15 US-10-128-714-4018		5.0	92.5	20
Sequence 12967, A	9 US-09-815-242-12967		5.0	93 .	19
Sequence 5816, Ap	9 US-09-815-242-5816		5.0	93	18
e 567	10 US-09-738-626-5676		5.0	93	17
Sequence 12703, A	9 US-09-815-242-12703		5.0	93	16

ALIGNMENTS

Q В δÃ ; TYPE: PRT ; ORGANISM: Streptomyces avermitilis US-10-156-761-10098 밁 RESULT 1 US-10-156-761-10098 PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 10098
LENGTH: 385 Query Match 43.3 Best Local Similarity 44.9 Matches 164; Conservative GENERAL INFORMATION: Sequence 10098, Application US/10156761 Publication No. US20030119018A1 APPLICANT: APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, SOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262 PRIOR APPLICATION NUMBER: JP 2001-204089 PRIOR FILING DATE: 2001-05-30 CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29 APPLICANT: OMURA, SATOSHI APPLICANT: IKEDA, HARUO APPLICANT: 77 DADALAVIARKSQIPVIADIHFQPKYVFAAIEAGCAAVRVNPGNIKQFDDKVKEIAKAAK 83 17 .00 AAEAFKLIKQQVNVPLVADIHFDYRIALKVAEYGVDCLRINDGNIGN-EERIRMVVDCAR 126 QRRKSTRIYVGNVPIGDGAPIAVQSMTNTRTTDVEATVNQIKALERVGADIVRVSVPTMD ERRKSRQIQVGTVAVGGDAPVSVQSMTTTRTSDIGATLQQIAELTASGCQIVRVACPTQD ISHIKAWA, JUN HORIKAWA, HIROSHI HARUO 43.3%; 70; Score 808; DB 15; Pred. No. 1.9e-74; 0; Mismatches 119; DB 15; L.9e-74; Length Indels 12; Gaps 76 67

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366 AEQME 370

RESULT 2 US-09-881-752A-196

Sequence 196, Application Patent No. US20020115078A1

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GENERAL INFORMATION:

APPLICANT: Kleanthous, Harc APPLICANT: Al-Garawi, Amal

Harc

APPLICANT:

Miller, Charles

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303 ALGEAKHADMAIAFGNRSGLIIKEGKVIHKLAEKDLFETFVIEVENLAKEREKS

356

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APPLICANT: Tomb, Jean-Francois
APPLICANT: Oomen, Raymond P2
APPLICANT: Oomen, Raymond P2
TITLE OF INVENTION: Identif@Cation of Polynucleotides
TITLE OF INVENTION: Encoding No. US20020115078A1e1 Helicobacter Polypeptides in
TITLE OF INVENTION: Genome
TITLE OF INVENTION: Genome
FILE REFERENCE: 06132/041002
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Pred. No. 4.7e-73;
3; Mismatches 117
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US-09-738-626-5705
; Sequence 5705, Application US/09738626
; Publication No. US20020197605A1
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              GENERAL INFORMATION:
APPLICANT: NAKAGKWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSI
APPLICANT: ANDO, SEIKO
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PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 9186
LENGTH: 385
TYPE: PRT
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Best Local
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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
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CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
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APPLICANT:
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                                                                                                                                                                                                                                                                                             PVEEIKVGIQILESLGLRQRRLEIVSCPSCGRAQVDVYKLAEEVTAGLEGMEVPLRVAVM
                                                                                                                                                                                                                                                                                                              PVEEIKVGFDILKSLRIRSRGINFIACPTCSRQEFDVIGTVNALEQRLEDIITPMDVSII 303
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HORIKAWA, HIROSHI
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SAKAKI, YOSHIYUKI
                              MIZOGUCHI, HIROSHI
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   HAYASHI,
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Pred. No. 3.1e-7
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; TYPE: PRT ; ORGANISM: Helicobacter py US-09-881-752A-196

SOFTWARE: FastSEQ for Windo SEQ ID NO 196 LENGTH: 359

PRIOR APPLICATION NUMBER: UPRIOR FILING DATE: 1997-04-NUMBER OF SEQ ID NOS: 370 CURRENT APPLICATION NUMBER: CURRENT FILING DATE: 2001-

Query Match Best Local S Matches 162

Local Similarity

162;

Conservative

73;

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RESULT 5
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              CURRENT APPLICATION NUMBER: US/09/712,363
CURRENT FILING DATE: 2000-11-13
PRIOR APPLICATION NUMBER: PCT/US00/02246
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/179,531
PRIOR FILING DATE: 2000-02-01
PRIOR APPLICATION NUMBER: 60/117,844
PRIOR FILING DATE: 1999-01-29
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; LENGTH: 378
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-5705
                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                  Sequence 256, Application US/09712363 Patent No. US20020164588A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                        TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS FILE REFERENCE: 07419-032001
                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                        APPLICANT: Elsenberg, David
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PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
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CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
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  APPLICATION
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Marcotte, Edward M.
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SENOH, AKIHIRO
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NUMBER: 60/118, 206,
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Pred. No. 1.3e-69;
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US-10-156-761-10088
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                                                                                                                                                                                                                                                                                                                                Sequence 10088, Application US/10156761 Publication No. US20030119018A1
                                                                                 APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
        PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                               APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
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ISHIKAWA, JUN HORIKAWA, HIROSHI SHIBA, TADAYOSHI

NOS:

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; ORGANISM: Mycobacterium tuberculosis US-09-712-363-256
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LENGTH: 387
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PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 60/134,093
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/134,092
PRIOR FILING DATE: 1999-05-14
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368 EMGEQ 372
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                                           QQVEK 372
                                                                                      NGPGEAREADLGVASGNGKGQIFVRGEVIKTVPEAQIVETL---
                                                                                                                               NGPGEALVSTLGVTGGNKKSGLYEDGVRKDRLDNNDMIDQLEARIRAKASQLDEARRIDV 367
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                                                                                                                                                                               VKVGNQVLESLNLRPRSLEIVSCPSCGRAQVDVYTLANEVTAGLDGLDVPLRVAVMGCVV
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Pred. No. 1.
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; LENGTH: 1046
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-10088
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                                  APPLICATION NUMBER: 09/1
FILING DATE: 29-UNW-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David T
                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS TITLE OF INVENTION: THERAPY OF EHRLICHIA INFECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                       CLASSIFICATION:
                                                                                                                                                       FILING DATE:
                    REGISTRATION
                                                                                                                                                                             APPLICATION NUMBER: US/09/159,469
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REFERENCE/DOCKET
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ilarity 21.8%;
Conservative 4
                    David J.
| NUMBER:
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  BER: 31,392
NUMBER: 210121.439C2
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                                              ; TYPE: PRT
; ORGANISM: Ehrlichia
US-09-798-042-50
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                                                                                            CURRENT APPLICATION NUMBER: US/09/798,042
CURRENT FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 108
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 50
LENGTH: 578
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Best Local s
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                             Sequence 50, Application US/09798042 Patent No. US20020068343A1
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 578 amino acid
                                                                                                                                                                                                APPLICANT: Houghton, Raymond L.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF EHRLICHIA INFECTION
FILE REFERENCE: 210121.439C7
                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
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TELEPHONE: 206-622-4900
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   105.5; DB
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US-09-815-242-5635
                                                   SEQ ID NO 5635
LENGTH: 2368
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APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, Howard
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA,011A
FILE REFERENCE: ELITRA,011A
                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
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CURRENT FILING DATE: 2001-03-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Haselbeck, Robert
        ORGANISM: Staphylococcus
                                                                                                                                                                                                                APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
                                                                                                                                                                                             APPLICATION NUMBER: 60/257,931
                                                                                                                                                                                                                                                           FILING DATE: 2000-10-
                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/242,578
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                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/207,727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wall, Daniel
Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Onisen, Kari L.
Zyskind, Judith W.
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                                                                                                                                     DATE:
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                                                                                        Windows Version
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US-09-815-242-12389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12389, Application Patent No. US20020061569A1
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                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
                                                                                                                                                                                                                                                                                   FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
                                                                                                                        APPLICATION NUMBER: 60/253,625 FILING DATE: 2000-11-27
                                                                                                                                                                                    APPLICATION NUMBER: 60/242,578
                                                            APPLICATION NUMBER: 60/269,308
                                                                                 APPLICATION NUMBER: 60/257,931 FILING DATE: 2000-12-22
                                                                                                                                                                                                          FILING DATE: 2000-05-26
                                                                                                                                                                 FILING DATE: 2000-10-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ESYRLLA--KQIDQPLHLGITEAGGARSGAVKSAIGLGLLLSEGIG-DTLRVSLAADPVE 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EIKVGFDILKSLRIRSRGINFIACPTCSRQEFDVIGTVNALEQRLEDIITPMDVSIIGCV
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                                           DATE:
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for Windows Version
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2.9;
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US-09-815-242-12389
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US-10-156-761-8947
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LENGTH: 2368
TYPE: PRT
                                             ; ORGANISM: Streptomyces US-10-156-761-8947
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                                                                                                                                                                                                                                                                                                                               Sequence 8947, Application US/1
Publication No. US20030119018A1
                                                                                                NUMBER OF SEQ ID NOS:
SEQ ID NO 8947
Matches
                    Query Match
                                                                                                                                                                       APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUMA
APPLICANT: HATTORI, MASAHIMA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
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APPLICANT:
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                                                                        LENGTH: 365
TYPE: PRT
          Local
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77;
            Similarity
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HORIKAWA, HIROS
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Conservative
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DNA-VKEGKAKINAVKTFSEYKKDALAKIEAAYNAKVTEADNSN 1590
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54;
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                                                               itilis
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Pred. No.
         Score 98.5; DB 15; Pred. No. 0.17;
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                                                   ; ORGANISM: Haemophilus influenzae US-09-815-242-10969
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             Query Match
Best Local
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  . Similarity
85; Conserv
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Trawick, John D.
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Zyskind, Judith W.
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Xu, H. Howard
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    Conservative
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                5.1%;
     59;
      Mismatches
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 10969
LENGTH: 504
TYPE: PRT
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/269,308 FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/207,727
FILING DATE: 2000-05-26
APPLICATION NUMBER: 60/242,578
FILING DATE: 2000-10-23
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APPLICATION NUMBER: 60/257,931
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5. US20020061569A1
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                 Score 96;
Pred. No.
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                    DB 9;
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134;
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                                             Length 504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -DQGLVHAPA-GPGIALPLD 350
  Indels
     108;
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     Gaps
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     21;
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); ORGANISM: H. US-10-260-877-70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 70
LENGTH: 504
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 70, Application US/10260877 Publication No. US20030021813A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hessler, Paul E.
APPLICANT: Reich, Karl A.
TITLE OF INVENTION: ESSENTIAL BACTERIA GENES
TITLE OF INVENTION: SCANNING IN HAEMOPHILUS
TITLE OF INVENTION: 'ESSENTIAL GENES'
FILE REFERENCE: 6565.US.Pl
CURRENT APPLICATION NUMBER: US/10/260,877
CURRENT APPLICATION NUMBER: US/10/260,877
CURRENT TILING DATE: 2002-09-30
CURRENT TILING DATE: 2002-09-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US/09/649,145
PRIOR ETLING DATE: 2000-08-25
NUMBER OF FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Abbott Laboratories APPLICANT: Chovan, Linda E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                             Local
    185 VFLAVESYRLLAKQIDQPL-----HLGITEAGGARSGAVKSAIGLGLLLSEGIGD----
                                                                   136 QLGLGEIEQIAASQGRGVTQLMEQVLAP----FAEKMENADENDRTSEEEQDEWEQEFD
                                                                                                                   129
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                                                                                                                                                                82
                                                                                                                                                                                                  24 TRTRD--ALVADFPGLTRDRKYGHAHIAGYDFJVIDTGGIDGTEEGVEEKMAEQSLLAID
                                                                                                                                                                                                                                                                                     36 TRTTDVEATVNQIKALER-----VGADIVRVSVPTMDAAE---AFKLIKQQVNVPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84
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                                                                                                            NIPI----RIGVNAGSLEKDLQEKYGEPTPQALLESAMRHVDHLDRLNFDQFKVSVKASD
                                                                                                                                                         EADIVLELVDARAGLTAADIGIANYLR-----QRQNKITVVVANKTDGIDADSHCAEFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NNDMIDQLEARIRAKASQLDEARRID 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QLGLGEIEQIAASQGRGVTQLMEQVLAP----FAEKMENADENDRTSEEEQDEWEQEFD 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VADIHF --- DYRIALKVAEYGV-DCLRINPGNIGNEERIRMVV------DCARDK 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRTRD--ALVADFPGLTRDRKYGHAHIAGYDFIVIDTGGIDGTEEGVEEKMAEQSLLAID 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DANVVLLTIDARENISDQDLSLLGFILNA-GRSLVIVV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VFDMPGTTRDSIYI-PMERDGQQYTLIDTAGVRKRGKVHLAV----EKFSVIKTLQAIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----TLRVSLAADPVEEIKVGFDILKSLRIRSRGINFIACPTCSRQEFDVIGTVNALE 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -FDSEEDTALIDDALDEELEEEQDKNIKIAIVG-----RPNVGKSTLTNRILGEDRVV 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VFLAVESYRLLAKQIDQPL-----HLGITEAGGARSGAVKSAIGLGLLLSEGIGD----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EADIVLELVDARAGLTAADIGIANYLR-----QRQNKITVVVANKTDGIDADSHCAEFY 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRTTDVEATVNQIKALER-----VGADIVRVSVPTMDAAE---AFKLIKQQVNVPL 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chovan, Linda E.
Hessler, Paul E.
Reich, Karl A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   influenzae
                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----KSELD--RRLD 356
                                                                                                                                                                                                                                                                                                                                                           5.1%; Score 96; DB 15; Length 504; 22.0%; Pred. No. 0.51;
                                                                                                                                                                                                                                                                                                                                  59; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AND GENOME
                                                                                                                                                                                                                                                                                                                                       134; Indels
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US-09-815-242-5590
                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 63; Conserv
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SOFTWARE: FASTSEQ FOR WINDOV
SEQ ID NO 5590
LENGTH: 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5590, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Identification TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L. APPLICANT: Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/257, 931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/242,578 PRIOR FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/207,727 PRIOR FILING DATE: 2000-05-26
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APPLICANT:
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202 PLHLGITEAGGARSGAVKSAIGLGLLLLSEGIGD----TLRVSLAADPVEEIKVGFDILKS
                                                                     143
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                                                                                                                                                         120
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                                                                                                                                                                                                                                            60
                                                                                                                                                                                                                                                                   27 PIAVQSMTNTRTTDVEAT-----VNQIKALERVGADIVRVSVPTMDAAEAFKLIKQQVNV
                                                                                                                                                                                           PLVADIHEDYRIALKVAEYGVDCLRINPGNIGNEERIRMVVDCARDKNIPIRIGVNAGSL
                                                                 RTK-----GEPGTGNIVEA----VRHMRQVNSEVSRLTVMNDDEIMT-----FAKDIGA 187
                                                                                                          EKDLQEKYGEPTPQALLESAMRHVDHLDRLNFDQFKVSVKASDVFLAVESYRLLAKQIDQ
                                                                                                                                                                                                                                          PKIVEEVMNAVSIPVMAKARIGHITEARVLEAMGVDYIDESEVLTPADEEYHLRKDQFTV
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                                                                                                                                                         PFVCGCR---
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Yamamoto, Robert T.
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                                                                                                                                                                                                                                                                                                                                  Conservative
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RESULT 15
US-09-815-242-12428
; Sequence 12428, Application
; Patent No. US20020061569A1
Search completed: August 12,
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; DRCANISM: Staphylococcus
US-09-815-242-12428
                                                                                                                                                                                                                                                                              Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ
SEQ ID NO 12428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: (PRIOR FILING DATE: 2000-05)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               URRENT APPLICATION NUMBER: 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Identif
                                                                                                                                                                                                                                                                   Local Similarity 21.0 les 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER FILING DATE: 2000-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: (FILING DATE: 2000-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   238 -EDPEKFAKAIVQATTHYODYELIGRLASDLGTAMKGLDINGLSLEERMQE 287
                                     243 -EDPEKFAKAIVQATTHYQDYELIGRLASDLGTAMKGLDINQLSLEERMQE 292
                                                       258 LRIRSRGINFIACPTCSRQEFDVIG------TVN--ALEQRLED 293
                                                                                                                                                                            125
                                                                                                                                                                                         82 PLVADIHFDYRIALKVÄEYGVDCLRINPGNIGNEERIRMVVDCARDKNIPIRIGVNÄGSL 141
                                                                                                                                                                                                                     PFVCGCR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wall, Daniel
Trawick, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carr, Grant J.
Yamamoto, Robert
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ELITRA.011A
     2003, 10:07:05
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03-21
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                                                                                                                                                                                                                                                                  % Score 94.5; DB 9;
% Pred. No. 0.31;
35; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                               /253,625
                                                                                                                                                                                                                                                                                                                                                                    Version
                                                                                                                                                                             Length 295;
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                                                                                                                                                                            ----RIGEGAAML 147
                                                                                                                                                                                                                                                                   87;
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Job time : 58 secs

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Command line parameters:

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-Q-Cgn2_1/GSPTO_spool/US09921992/runat_12082003_094911_17364/app_query.fasta_1.519

-DB-GenEmbl -OFMT=fastap -SUFFIX=-rge -MINMATCH=0.1 -LOOPEL-0 -LOOPEXT=0

-UNITS=bits -START=1 -SUD-1 -MATRIX-blosum62 -TRANS-human40.cdi -LIST-45

-DCCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN-0 -ALIGN=15 -MODE_LOCAL

-OUTFMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-2000000000

-USER-US09921992_deGN 1_1_3508_crunat_12082003_099911_17364 -NCPU-6 -ICPU-3

-NO_MMAP -LARGEQUERY -NEC_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG

-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6

-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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3289.749 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Course Match Length DB ID 1866 100.0 1119 1 AN033515 AN033515 Escherich AN033516 Escherich AN033516 Escherich AN033516 Escherich AN033516 Escherich AN033516 Escherich AN033517 Escherich AN033518 Escherich AN033517 Escherich AN033518 Escherich A													•																														
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Best Local Similarity:
Query Match:
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Rohdich,F., Hecht,S., A
Direct Submission
Submitted (27-APR-2001)
Biochemie, Lehrstuhl II
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Proc. Natl. Acad. Sci.
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Enterobacteriaceae; Bscherichia.
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Hecht, S., Eisenreich W., Adam, P.
Arigoni, D. and Rohdlich, F.
Studies on the nonmevalonate pat
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                                              GlnProLeuHisLeuGlyIleThrGluAlaGlyGlyAlaArgSerGlyAlaValLysSer
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Location/Qualifiers
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Enterobacteriaceae; Escherichia.
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GlnProLeuHisLeuGlyIleThrGluAlaGlyGlyAlaArgSerGlyAlaVallysSer
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/mol_type="genomic DNA"
/db_xref="taxon:562"
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Qy 21 ProIleGlyAs Db 61 CCGATTGGCGA	Qy 1 MetHisasngl 	US-09-921-992-78 (1-372)	Alignment Scores: Pred. No.: 9 Score: 1 Percent Similarity: 1 Best Local Similarity: 1 Query Match: DB:	ORIGIN /ORG	AUTHORS LOFerer TITLE NOVel mi JOURNAL Patent: GPC BIO EATURES Source	ANISM	RESULT 3 AX038912 LOCUS AX038912 AX038912 DEFINITION Sequence 29 f ACCESSION AX038912 VERSION AX038912.1 G KEYWORDS	361 1081	Qy 341 AsnAsnAspM 	Qy 321 ThrGlyGlyAn Db 961 ACCGGCGCAN	Qy 301 Serileileg	281 841	781	241 Alaal 721 GCGGC	661
OIleGlyAspGlyAlaProIleAlaValGlnSermetThrAsnThrArgThrThrAs 	MetHisasnGlnalaProIleGlnArgArgLysSerThrArgIleTyrValGlyAsnVa 	x AX038912 (1-1119)	.1e-136 Length: .866.00 Matches: .00.00% Conservative: .00.00% Mismatches: .00.00% Indels: .00.00% Gaps:	Janısm="Escherichia coli" Ltype="genomic DNA" xref="taxon:562" 279 c 317 g 251 t	acobi,A. c identifying antibacteri 793-A 29 19-OCT-2000; (DE) : LOFERER HANNES (DE 07/Qualifiers	1 i obacteria; Gammaproteobac sae; Escherichia.	1119 bp DNA from Patent WO0061793. 31:11228221	GluAlaArgArgIleAspValGlnGlnValGluLys 37 	ASDASPMETILEASPGIDLEUGIUAlaArgIleArgAlaLySAlaSerGIDLEUAS 	ThrGlyGlyAsnLysLysSerGlyLeuTyrGluAspGlyValArgLysAspArgLeu 	SerIleIleGlyCysValValAsnGlyProGlyGluAlaLeuValSerThrLeuGlyVal 	IleGlyThrValAsnAlaLeuGluGlnArgLeuGluAspIleIleThrProMetAspVal 	lyIleAsnPheIleAlaCysProThrCysSerArgGlnGluPheAspVa1 	aAspProValGluGluILeLysValGlyPheAs 	GCCATTGGTTTAGGTCTGCTGTCTGAAGGCATCGGCGACACGCTGCGCGTATCGCTG
tThrAsnThrArgThrThrAsp 40 	rArgileTyrValGlyAsnVal 20 		11119 372 0 0		al compounds)) ; JACOBI ALEXANDER (DE)	teria; Enterobacteriales;	linear paT 16-NOV-200	116	gAlaLysalaSerGlnLeuAsp 360 	YVALATGLYSASPATGLEUASP 340 	laLeuValSerThrLeuGlyVal 320 	3PIleIleThrProMetAspVal 300 	/SSerArgGlnGluPheAspVal 280 	LysValGlyPheAspIleLeuLysSerLeuArgIle 260 	SCGACACGCTGCGCGTATCGCTG 720

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ValGluAlaThrValAsnGlnIleLysAlaLeuGluArgValGlyAlaAspIleValArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTGCCGCTGGTGGCTGACATCCACTTCGACTATCGCATTGCGCTGAAAGTAGCGGAATAC
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                                                                 CGTTCGCGAGGGATCAACTTCATCGCCTGCCCGACCTGTTCGCGTCAGGAATTTGATGTT
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                                            GluAlaArgArgIleAspValGlnGlnValGluLys
                                                                                               ACCGGCGGCAACAAGAAAAGCGGCCTCTATGAAGATGGCGTGCGCAAAGACCGTCTGGAC
                                                                                                      ThrGlyGlyAsnLysLysSerGlyLeuTyrGluAspGlyYalArgLysAspArgLeuAsp
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  from
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  1119 bp
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Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Escherichia.
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AX050487.1
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for altering the concentration of isopreno
patent: WO 0072022-A 1 30-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                     CCGATTGGCGATGGTCCCCATCGCCGTACAGTCCATGACCAATACGCGTACGACAGAC
                                                                                                                                                                                                                                                                                                                  {\tt LeuGluLysAspLeuGlnGluLysTyrGlyGluProThrProGlnAlaLeuLeuGluSer}
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a 279 c 317 g 251 t
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                                                                                   Boronat,A., Campos,N., Rodriguez-Concepcion,M., Seeman,M., Valentin,H.E., Venkatesh,T.V. and Ven Methyl-d-erythritol phosphate pathway genes Patent: WO 0212478-A 3 14-FEB-2002; Monsanto Technology LLC (US) Location/Qualifiers
                                                                                                                                                                            Escherichia coli
Escherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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Venkatramesh, M.
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¥ 0	al Similarity: 100.00% Mismatches: tch: 100.00% Indels: 6 Gaps:
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Qy	1 MetHisAsnGlnAlaProIleGlnArgArgLysSerThrArgIleTyrValGlyAsnVal 20
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Qy	21 ProIleGlyAspGlyAlaProIleAlaValGlnSerMetThrAsnThrArgThrThrAsp 40
Db	61 CCGATTGGCGATGGTGCTCCCATCGCCGTACAGTCCATGACCAATACGCGTACGACAGAC 120
Qy	41 ValGluAlaThrValAsnGlnIleLysAlaLeuGluArgValGlyAlaAspTleValArg 60
Db	1 GTCGAAGCAACGGTCAATCAAATCAAGGCGCTGGAACGCGTTGGCGCTGATATCGTCCG
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Qy	81 ValProLeuValAlaAspIleHisPheAspTyrArgIleAlaLeuLysValAlaGluTyr 100
Db	241 GTGCCGCTGGTGGCTGACATCCACTTCGACTATCGCATTGCGCTGAAAGTAGCGGAATAC 300
Qy	101 GlyValAspCysLeuArgIleAsnProGlyAsnIleGlyAsnGluGluArgIleArgMet 120
Db	301 GGCGTCGATTGTCTGCGTATTAACCCTGGCAATATCGGTAATGAAGAGCGTATTCGCATG 360
Qy	121 ValValAspCysAlaArgAspLysAsnIleProIleArgIleGlyValAsnAlaGlySer 140
Ъ	361 GTGGTTGACTGTGCGCGCGATAAAAAACATTCCGATCCGTATTGGCGTTAACGCCGGATCG 420
Qy	141 LeuGluLysAspLeuGlnGluLysTyrGlyGluProThrProGlnAlaLeuLeuGluSer 160
Db	421 CTGGAAAAAGATCTGCAAGAAAAGTATGGCGAACCGACGCCGCAGGCGTTGCTGGAATCT 480
Qy	161 AlaMetArgHisValAspHisLeuAspArgLeuAspPheAspGlnPheLysValSerVal 180
Db	481 GCCATGCGTCATGTTGATCTCGATCGCCTGAACTTCGATCAGTTCAAAGTCAGCGTG 540
. Qy	181 LysalaSerAspVa1PheLeuAlaValGluSerTyrArgLeuLeuAlaLysGlnIleAsp 200
Db	541 AAAGCGTCTGACGTCTTCCTTCGCTGTTGAGTCTTATCGTTTGCTGGCAAAACAGATCGAT 600
Qy	201 GlnProLeuHisLeuGlyIleThrGluAlaGlyGlyAlaArgSerGlyAlaValLysSer 220
Db	601 CAGCCGTTGCATCTGGGGATCACCGAAGCCGGTGGTGCGCGCAGCGGGGCAGTAAAATCC 660
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X64451.S43432
X64451.1 GI:41540
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2 (bases 1 to 1697)
Baker, J., Franklin, D.B. and Parker, J.
Sequence and characterization of the FEMS Microbiol. Lett. 94, 175-180 (19 See also J01629 & M11843.
                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (17-FEB-1992) J. Parker,
Submitted (17-FEB-1992) J. Parker,
Submitted (17-FEB-1992) J. Parker,
                                                                                                                                                                                                                                                                                                                                                                                                               gcpE gene.
Escherichia coli
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Enterobacteriaceae; Escherichia.
1 (bases 1 to 1697)
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                                                     AlaIleGlyLeuGlyLeuLeuSerGluGlyIleGlyAspThrLeuArgValSerLeu
                                                                                    GlnProLeuHisLeuGlyIleThrGluAlaGlyGlyAlaArgSerGlyAlaValLysSer
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Matches:
Conservative:
Mismatches:
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Gaps: 1697 372 0 0 0 60 20 774 80 654 40 594 160 954 140 894 834 100 714

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Perna, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D., Rose, D.J., Mayhew, G.F., Evans, P.S., Gregor, J., Kirkpatrick, H.A., Posfal, G., Hackett, J., Klink, S., Boutin, A., Shao, Y., Miller, L., Grotbeck, E.J., Davis, N.W., Lim, A., Dimalanta, E., Potamousis, K., Apodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C., Welch P. A., Panden, P. S., Lin, J., Yen, G., Schwartz, D.C.,
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                                                                                                                                                                                                                                                                                              Submitted (22-OCT-2000) Laboratory of Genetics, Usawisconsin, 445 Henry Mall, Madison, WI 53706, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli 0157:H7 EDL933
Escherichia coli 0157:H7 EDL933
Ranteria: Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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  pct identical
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                                                                                                                                                                                                                                                                                                                 of.
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ribonucleotide biosynthesis"
//note="Residues 1 to 143 of 143 are 100.00 pct identical to residues 1 to 143 of 143 from Escherichia coli K-12 Strain MG1655: B2518"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="orf, hypothetical protein"
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RVETVIIPEDDRATLCVSQVCGALECKFCSTAQOGENRULRVSEIIGQVWRAAKIVG
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LDKLGDWIDVALAISLHAAPUDEIRDEIVPINKXXNXESTFLAAVTRSTSKANGGRVT
IEXVMLDHVNDGTEHAHQAELLKDTPCKINLIPWPEPPAAPYGRSSMSRIDRFSKVL
MSYGFTTIVRKTRGDDIDAAGGQLAGDVIDRTKRTLRKRMQGEAIDIKAV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MG1655: B2517"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product-"putative membrane protein"
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/db_xref-"Gi:12516910"
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/translation-"MNTEATHDONEALTTGARLRNAREOLGLSQQAVAERLCLKVSTV
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/translation-"MNTEATHDONEALTTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYTALOGUESYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(3833. .4264)
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AMRHVDHLDRLMFDDFKYSVEKASDVPLAVESYRLLAKQIDDPLHLGTTEAGGARSGAV
KSAIGIGLLLSEGIGDTLRVSLAADPVEEIKVGFDILKSLRIRSRGINFIACPTCSRQ
EFDVIGTVNALEGGREDIITPMDVSIIGCVVNGGPGEALVSTLGVTGGNKKSGLYEDGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(3833. .4264)
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                                                                                                                                                                                                                                                                      transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'gene="ndk"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="synonym: Z3781"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="ndk"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /function="orf; Unknown function"
/note="Residues 1 to 384 of 384 are 99.47
residues 1 to 384 of 384 from Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(2529. .3683)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGMQRKDGNLNLTGQAPYKLKIGAPAAVQIQYQGKPVDLSRFIRTNQVARLTLNAEQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              residues 1 to
MG1655: B2516"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /function="putative membrane; Not classified"
/note="Residues 1 to 337 of 337 are 99.10 pct
residues 1 to 337 of 337 from Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(1231. .2244)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        function="enzyme; Nucleotide biosynthesis: Purine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(1231. .2244)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RKDRLDNNDMIDQLEARIRAKASQLDEARRIDVQQVEK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ′transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'gene="yfgA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="yfgA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pct identical to coli K-12 Strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    identical to
i K-12 Strain
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                                                                                                                                                                                                                                                                                                                                      CDS
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/transl_table=11
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GQLKPIITLSWGISVIGMMFFAVGGCKKNIPAALFGSVMLVGSEVMLRFVFFSIG"
complement(6073...6510)
/gene="23784"
complement(6073...6510)
/gene="23784"
/function="putative enzyme; Not classified"
/note="Residues 4 to 134 of 145 are 61.83 pct identical to
/note="Residues 4 to 134 of 125 from GenPept 118:
    residues 57 to 186 of 205 from GenPept 118:
    gill787122|gb|AAC73981.1| (AE000191) anaerobic dimethyl
sulfoxide reductase subunit B [Escherichia coli]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /function="putative enzyme; Not classified"
/note="Residues:2 to 272 of 273 are 25.26 pct identical
residues 6 to 276 of 286 from GenPept 118 :
gi|5002126|gb|AAD37317.1|AF135170_8 (AF135170) dimethyl
sulfoxide reductase subunit C [Yersinia pestis]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="Z3782"
complement(44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAG57629.1"
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/db_xref="G1:12516913"
/db_xref="G1:12516913"
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SPHTSEVNVSRRRLFHVQRADVQMTQIQPGLRRLHYLWPQISDARPMMDPQKCQLCGA
CWRACEQQVFSLNEGHLQINDALCNGCQNCIAVCFHQAMTVELTILPAKIVNLHANRK
VCKTQCKSFLTFQQNAQNCLYCQRHRYGMRTP"
complement(5259..6080)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="0-island #106; Region of the EDL933 chromosome
homologous to E. coli K-12 MG1655"
complement(4405. .4983)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LRADYADSLTENGTHGSDSVESAAREIAYFFGEGEVCPRTR" 4397. 9255
                                           /product="putative dimethyl sulfoxide reductase subunit A"
/protein_id="AAG57632.1"
/db_xref="G1:1516916"
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SPEVTAPVADKVVPTCSTFDCGGKCDIRAHMRDGVVTQITTLPDNELDPQMPIMRACV
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//gene="23785"
/function="putative enzyme; Not classified"
/function="putative 792 of 793 are 43.59 pct identica
/note="Residues 25 to 792 of 793 are 43.59 pct identica
to residues 3 to 784 of 785 from GenPept 118 :
gi|1787121|gb|AAC73980.1| (AE000191) anaerobic dimethyl
sulfoxide reductase subunit A [Escherichia coli]"
                                                                                                                                                                                                                                                                                                                                                   /translation="MSHNVFAYTLSVSCNHCADPICTKNCPTMAMHKRPGDGIVRVNT
DKCYCGYCAWSCPYGAPQMBQTGXXSKCDFCIDLQAKGEQPICVATCPLGAIKFGP
IDELREKYGDVSDVKGLPDSSITQPNLVIKPHQGAEKEASHHA"
complement(6699. 9080)
/gene="Z3785"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(5259. .6080)
/gene="Z3783"
RGRGYRKFVYHPDRLKYPMKRVGKRGEGKFERISWDEATTLIADNLKRITQQYGPASR
YVHVGTAVXGGTFSGDAMARRLLNLTGGYLEYYHSVSLGNTAAATPYTYGVAASGNSM
                                                                                                                                                                                                                                                                                                                                   complement(6699. .9080)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="putative dimethyl sulfoxide reductase
/protein_id="AAG57631.1"
/db_xref="GI:12516915"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /function="orf; Unknown function"
/note="No significant matches"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="Z3782"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transl_table=11/
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DGIHKTPEWAEKITHVEAQSIRQLARDYATTKEAALIQGWEPQRHIGGERTARGSTTL
ASITGNVGIKGGWAAGYGGSSNRKFCVGFDMPENPVQAKISIMWWQAADDAKKVTPQ
DGLKGVDKLDSNIRLLFSLAGNYLAHQANDDVHQAAKLLEDESKIEFIVLSDLFMTPSA
KYADVLLPETSEWERWNIGETWGTASYLILSEKPIEPDFERRTDYDWLADVAKKLGVE
AEFSQGRDEKQWIEHIWEQTRLAMPDENLPDFATLQKTRRHLFKSAPHIAFEANIRDF
QNNDFFTPSGKIEIFSKRLETMODDEIFALSHYVDAFEEGFEDKLTAKYFLQLITWKGK
NRANSTQYANPWLQEVQTQKLWLNPQDAKQRGISEGDSVKIYNDRGVSIIPVEITPRI

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US-09-921-992-78 (1-372) x AE005481 (1-11521)
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                         LeuGluLysAspLeuGlnGluLysTyrGlyGluProThrProGlnAlaLeuLeuGluSer
                                                                                                                                                                                                                                                                                                                             GTGGTTGACTGTGCGCGCGATAAAAACATTCCGATCCGTATTGGCGTTAACGCCGGATCG
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                                    AlaIleGlyLeuGlyLeuLeuLeuSerGluGlyIleGlyAspThrLeuArgValSerLeu
                                                                                                                                             GlnProLeuHisLeuGlyIleThrGluAlaGlyGlyAlaArgSerGlyAlaValLySSer
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ArgSerArgGlyIleAsnPheIleAlaCysProThrCysSerArgGlnGluPheAspVal
                                                                                   GCCATTGGTTTAGGTCTGCTGCTGTCTGAAGGCATCGGCGACACGCTGCGCGTATCACTG
                                                                                                                                  AAAGCGTCTGACGTCTTCCTCGCTGTTGAGTCTTATCGTTTGCTGGCAAAACAAATCGAT
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AE000338
                                                                                                                                                                                                     Direct Submission
Submitted (13-0CT-1998) Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA
Wisconsin, 445 Henry Mall, Madison, WI 53706, USA
This sequence was determined by the E. coli Genome Project at the University of Wisconsin-Madison (Frederick R. Blattner, director). Supported by NIH grants H600301 and H601428 (from the Human Genome Project and NCHGR). The entire sequence was independently determined from E. coli K12 strain M61655. Predicted open reading than the Coli K12 strain M61655. Predicted open reading the frame was accommended from E. coli K12 strain M61655.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (16-JAN-1997) Guy Plunkett III, Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
Email: ecoll@genetics.wisc.edu Phone: 608-262-2534 Fax:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 13176)
1 (bases 
frames were determined using GeneMark software, kindly supplied by Mark Borodovsky, Georgia Institute of Technology, Atlanta, GA, 30332 [e-mail: mark@amber.gatech.edu]. Open reading frames that have been correlated with genetic loci are being annotated with CG Site Nos., unique ID nos. for the genes in the E. coli Genetic Stock Center (CGSC) database at Yale University, kindly supplied by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (02-SEP-1997) Guy Plunkett III, Laboratory of Genetics University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Blattner, F.R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCGGCGGCAACAAGAAAAGCGGTCTCTATGAAGATGGCGTGCGCAAAGACCGTCTGGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCGATTATCGGCTGCGTGAATGGCCCCGGGTGAGGCGCTGGTTTCTACACTCGGCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SerIleIleGlyCysValValAsnGlyProGlyGluAlaLeuValSerThrLeuGlyVal 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ## ATCGGTACAGTTAACGCGCTGGAGCAACGCCTGGAAGATATCATCACTCCGATGGACGTT
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Mary Berlyn. A public version of the database is accessible (http://cgsc.biology.yale.edu). Annotation of the genome is an ongoing task whose goal is to make the genome sequence more useful by correlating it with other data. Comments to the authors are appreciated. Updated information will be available at the E. coli Genome Project's World Wide Web site (http://www.genetics.wisc.edu). *** The E. coli Kl2 sequence and its annotations are periodically updated; this is version M54. No sequence changes. Annotation updates: updated gene identifications and products; all new functional assignments courtesy of Monica Riley; added promoters, protein binding sites, and repeated sequences described in reference 1. The unique numeric identifiers beginning with a lowercase 'b' assigned to each gene (protein or RNA-encoding) are now designated as gene synonyms instead of labels. This should allow them to be searched for in Entrez as gene names.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="factor Sigma70; promoter hisS; documented +1 at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:83333"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Escherichia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'function="orf; Unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sub_strain="MG1655"/
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l to YFGA_ECOLI
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/note="factor Sigma70; px
complement(3833. .4264)
/gene="ndk"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="synonym: b2519" complement(4413. .6725)
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/note="factor Sigma70; predicted +1 start at 2642935"
/complement(4413. .6725)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAKYTGORPITNUYMMGMGEPLLNILNUVPAMEIMLDDFGFGLISKRKYTLSTSGVVPA
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                                                                                   complement(6726. .11687)
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LNRAPFGGTLQGIGAASWAYLGKSPANLSYSEAAMLAVLPQAPSRLRPDRWPERAEAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene-"pbpC"
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/function-"putative enzyme; Not classified"
/note-"f170; This 770 aa ORF is 31 pct identical (43 gaps)
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complement(3833. .4264)
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                                                                                                                                                                                                            PYGHDAQLPLQLTGVRDGAIIKRLPGAAEATLPLQSSGGAGERWWFLNGEPLTERGRN
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/note="f143; 100 pct identical to NDK_ECOLI SW: P24233
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note="f1653;
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f1653"
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/translation="MKLRVAACMLMLALAGCDNNDNAPTAVKKDAPSEVTKAASSEN
/translation="M
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                                          Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12 DNA Res. 8 (1), 11-22 (2001)
                                                                                                         Hayashi,T., Makino,K., Ohnishi,M., Kurokawa,K., Ishii,K., Yokoyama,K., Han,C.-G., Ohtsubo,E., Nakayama,K., Murata,T., Tanaka,M., Tobe,T., Iida,T., Takami,H., Honda,T., Sasakawa,C. Ogasawara,N., Yasunaga,T., Kuhara,S., Shiba,T., Hattori,M. ar Shinagawa,H.
                                                                                                                                                                                                                                                                              Complete nucleotide sequence of the prophage VTI-Sakai carrying the Shiga toxin 1 genes of the enterohemorrhagic Escherichia coli 0157:H7 strain derived from the Sakai outbreak Gene 258 (1-2), 127-139 (2000)
                                                                                                                                                                                                                                                                                                                                                                                   Yokoyama,K., Makino,K., Kubota,Y., Watanabe,M., Kimura,S., Yutsudo,C.H., Kurokawa,K., Ishii,K., Hattori,M., Abe,H., Ii. Yamamoto,K., Hayashi,T., Yasunaga,T., Honda,T., Sasakawa,C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Comparative analysis of the whole set of rRNA operons between an enterohemorrhagic Escherichia coli 0157:H7 Sakai strain and an Escherichia coli K-12 strain MG1655
Syst. Appl. Microbiol. 23 (3), 315-324 (2000)
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Escherichia coli O157:H7 DNA, cc
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Kurokawa,K., Yasunaga,T., Yokoyama,K., Makino,K., Shinagawa,H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete nucleotide sequence of the prophage VT2-Sakai carrying the verotoxin 2 genes of the enterohemorrhagic Escherichia coli 0157:H7 derived from the Sakai outbreak Genes Genet. Syst. 74 (5), 227-239 (1999)
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T., Honda,T.,
                                                                                                                              Hattori, M. and
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be,H., Iida,T.,
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                                                                                                                                                                                                                                                                                                                complement(2789. .4147)
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                                                                                                                                                                                                                                                                                                                                                        complement(2789. .4147)
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Kurokawa,K.,
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mular to GLPA_ECOLI gi|1788574
man (Conserved in E.coli K-12)
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bable=11
Manaerobic sn-glycerol-3-phosphate dehydrogenase
subunit
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milar to YFAD_ECOLI gi|1788577 percent identity as but differs at C-ter (Conserved in E.coli
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27	\$=5	201 2797 4 6	Qy Db
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DIVIES NUNCLESTRY VELGGINHLEAR FPEHPHPLFY FREAHFQAQLQRLHETSFEKFFLTRADLALAHQHWEF LLLDEGHVTLDLWFGDINELTSQLDDSLNQKVDAWFF RLARPGSTLATFTSAGFVRRGLQEAGFTMOKRKGFGG RLARPGSNKQEAAITGGGTASALLSLALLRRGWQVTLY		AE016764 AE016764 AE016764 300099 bp DNA linear BCT 24-DEC-2002 DEFINITION Escherichia coli CFT073 section 10 of 18 of the complete genome. ACCESSION AE016764 AE014075 VERSION AE016764.1 GI:26109116	. < > m + +
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5log: z3590"
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"PEALN"
- 5338)
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nolog: z3587"
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plog: z3589"
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QFLGARMGSRLVISKQQKLIRPMIVIVSAVMSAKLLYDSHGQEILHWLGMN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="aroC"
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                   ERVLYPRSPIGELINNKFAGLISKOPOHILDMCTGSGCIAIACAYAFPEAEVDAVDIS
PDALAVAEQNIEEHGLIHNVIPIRSDLFRDLFKVQYDLIVTNPPYVDAEDMSDLPNEY
RHEPELGLASGTDGLKLTRRILGNAADYLADDGVLICEVGNSMVHLMEQYPDVPFTWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(7286. .8551)
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/transl_table=11
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301 SerIleIleGlyCysValValAsnGlyProGlyGluAlaLeuValSerThrLeuGlyVal 320 	1 30 1 18	261 ArgSerArgGlyIleAsnPheIleAlaCysProThrCysSerArgGlnGluPheAspVal 280 	SerLeuArgIle 26		18	181 LysalaSerAspValPheLeuAlaValGluSerTyrArgLeuLeuAlaLysGlnIleAsp 200 	161 AlaMetArgHisValAspHisLeuAspArgLeuAsnPheAspGlnPheLysValSerVal 180 	141 LeuGluLysAspLeuGlnGluLysTyrGlyGluProThrProGlnAlaLeuLeuGluSer 160 	AlaGlySer 1 GCCGGATCG 1	101 GlyValAspCysLeuArgIleAsnProGlyAsnIleGlyAsnGluGluArgIleArgMet 120 	81 ValProLeuValAlaAspIleHisPheAspTyrArgIleAlaLeuLysValAlaGluTyr 100 .	17 - 20	41 ValGluAlaThrValAsnGlnIleLysAlaLeuGluArgValGlyAlaAspIleValArg 60 	21 ProlleglyAspGlyAlaProlleAlaValGlnSerMetThrAsnThrArgThrThrAsp 40 	1 MetHisasnGlnalaProIleGlnargArgL 	ggnment Scores: 1.47e-132 Length: 300099 gd.No.: 1866.00 Matches: 372 re: 1866.00 Matches: 372 reent Similarity: 100.00% Conservative: 0 gry Match: 100.00% Mismatches: 0 ary Match: 100.00% Indels: 0 gaps: 0 gaps: 0 conservative: 0 gaps: 0 conservative:

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AUTHORS
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Nucleic Acids Res. 30 (20), 4432-4441 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (08-MAY-2001) Microbial Genome Center of Chinese Ministry of Public Health, 100 YingXin Jie, XuanWu Qu, Beijing 100052, P.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shigella flexneri 2a str. 301
Shigella flexneri 2a str. 301
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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AE015271 AE005674
AE015271.1 GI:24
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Shigella flexneri 2a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GluAlaArgArgIleAspValGlnGlnValGluLys 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AACAACGATATGATCGATCAGCTGGAAGCGCGCATTCGTGCGAAAGCCAGTCAGCTGGAC 187331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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a str. 301
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DEPGLITADRKYGRAELEGREFICIDTGGIDGTEDGVETRMAEOSILAIEEADVVLFMV
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                                                                                                                                                                                                                                                                                                     VLMEQGQMIWQQRISQATGSTEIDRLSDVDTTPVVVNGVVFALAYNGNLTALDLRSGQ
IMWKRELGSVNDFIVDGNRIYLVDQNDRVMALTIDGGVTLWAQSDLLHRLLTSPVLYN
GNLVVGDSEGYLHWINVEDGREVAQQKVDSSGFQTEPVAADGKLLIQAKDGTVYSITR
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complement(3311. .4489)
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complement(1721. .3232)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene≖"yfg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /locus_tag="SF2556"
/note="Residues 1 to 83 of 83 are 97
residues 1 to 83 of a 83 aa protein f
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/gene="yfgJ"
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/protein_id="AAN44056.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'gene="yfgK"
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/protein_id="aan44060.1"
/db_xref="GI:24052934"
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/translation="makan(palargmnDyLpGETAIWQRIEGTLKNVLGSYGYSEIRLP
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QRLWYIGPMFRHERPQKGRYROFHQLGCEVEGLOGPDIDAELINLTARWWRALGIFEH
QRLWYIGPMSIGSLEARANYRDALVAFLEOGHEKELLDECKRRWYTNDLRCVLDSKNPEVQAL
LNDAPALGDYLDEESREHFAGLCKLLESAGIAYTVNQRLVRGLDYYNRTYFEWYTNSL
GSQGTVCAGGRYDGLVEGLGGRAIPAVCFAMGLERLVLLVQAVNPEFKADPVVDITLV
ASGADTQSAMALAERRLPELLGVKLWINHGGGNFKKQFARADKWGARVAVVLGESEV
ANGTAVVKDLRSGEQTAVAQDSVAAHLRTLLG"
complement (6515. .7642)
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HQVDSarsaslayqnavtavsegkpdsipaaekfaaenkntygalaslelaqqfydkn
ELEKAAAQLQQGLADTSDENLKAVINLRLARVQVQLKQADAALKTLDTIKGEGWAAIV
ADLRGEALLSKGDKQGARSAWEAGVKSDVTPALSEMMQMKINNLSI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /transl_table=11
/product="orf, conserved hypothetical protein"
/product="orf, cancuserved hypothetical protein"
/protein_id="AAN4061.1"
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/locus_tag="SF2561"
complement(6515..7642)
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/locus_tag-"SF2560"
/note="Residues 1 to 424 of 424 are 99 pct identical to residues 1 to 424 of a 424 aa protein from Escherichia coli 0157:H7 EDL933 ref: NP_289067.1"
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DTAATPYPTAATTPDGAAPLPTDQAGVTTPAADPNALVMNFTADCWLEVTDATGKKLF
                                                                                                                                                                                                                                                                                                                                         /note-"Residues 1 to 337 of 337 are 99 pct residues 1 to 337 of a 337 aa protein from coli 0157:H7 ref: NP_311405.1"
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/transl_table=11
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/locus_tag="SF2562"
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                                                                             ArgSerArgGlyIleAsnPheIleAlaCysProThrCysSerArgGlnGluPheAspVal
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          ATCGGTACGGTTAACGCGCTGGAGCAACGCCTGGAAGATATCATCACTCCGATGGACGTT
                                                                                                                                                                                                           IleGlyThrValAsnAlaLeuGluGlnArgLeuGluAspIleIleThrProMetAspVal
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Complete Genome Sequence and Comparative Genomics of Shigella flexneri Serotype 2a Strain 2457T
Infect. Immun. 71 (5), 2775-2786 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wisconsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shigella flexneri 2a str. 2457T
Shigella flexneri 2a str. 2457T
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Shigella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genome.
AE016987 AE014073
AE016987.1 GI:30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shigella flexneri 2a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AsnAsnAspMetIleAspGlnLeuGluAlaArgIleArgAlaLysAlaSerGlnLeuAsp 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAAGCGCGTCGAATTGACGTTCAGCAGGTTGGAAAA 6527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCGGCGGCAACAAGAAAGCGGCCTCTATGAAGATGGCGTGCGCAAAGACCGTCTGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AACAACGATATGATCGACCAGCTGGAAGCACGCATTCGTGCGAAAGCCAGTCAGCTGGAC 6563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 290380)
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residues 1 to 372 of 372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (13-JUN-2002) Genetics Laboratory, University of Madison, 445 Henry Mall, Madison, WI 53706, USA
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2457T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /locus_tag="S2735"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(2534.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="truncated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /locus_tag="S2737"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene-"pbpc"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="hypothetical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /locus_tag="S2735"
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Best Local S
Query Match:
                                                       Percent Similarity:
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                                                                                                                                   Alignment
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| MGGAATVTGALAFAINRGLNKRVKLFLCADNLISGNAFKLGDLITYRNGKKVEYNNT
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| ASQENEPTWRLPLAEFHRSQLPSNFAELNNTGSAAKTALGNDYHALFSFDDALAGRLLAS
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B2522"
/codon_start=1
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GGLTQIHPAPERVLGPRLEHPAVLDLLQRYBSPEKLASILGEKKLAAQLCKLAPRLGKR 
LAADIAQALAEGTVVVPGTNAAAVVLPRLALQLITLKKQRDEVALEVEQRVLAHPLYP 
VLTSMPGVGVRTAARLLTEVACRAFASAAHLAAYAGLAPVTRRSGSSIRGEHPSRRGN
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B2523"
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/product="enhancer of serine sensitivity"
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/note="residues 1 to
residues 4 to 261 of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /function="putative enzyme; Not classified"
/note="residues 1 to 427 of 427 are 92.50 p
residues 30 to 456 of 456 from Escherichia
                                                                                                                                                                                                                                                  complement(11521.
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/locus_tag="S2742"
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/locus_tag="S2742"
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/note="truncated"
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                                                                                                                                                                                             /gene="yfhJ"
/locus_tag="S2743"
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                                                             TCGATTATCGGCTGCTGGTGAATGGCCCAGGTGAGGCGCTGGTTTCTACACTCGGCGTC
                                                                                                                                                                                                      SerIleIleGlyCysValValAsnGlyProGlyGluAlaLeuValSerThrLeuGlyVal
                                                                                                                                                                                                                                                                                     CGTTCGCGAGGGATTAACTTCATCGCCTGCCCGACCTGTTCGCGTCAGGAATTTGATGTT
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/codon_start=1 /transl_table=11

note="RatA (gi|4583529)"

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FEATURES
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                                                                                                                                                                                                                                                                                                 This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistries or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one ml3 subclone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The analyses of ribosome binding sites and promoter binding sites were kindly provided by Heladia Salgado, Julio Collado-Vides and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EC numbers were kindly provided by Junko Yabuzaki and the Kyoto Encyclopedia of Genes and Genomes; http://www.genome.ad.jp/kegg/, and Pedro Romero and Peter Karp at EcoCyc; http://ecocyc.PangeaSystems.com/ecocyc/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Coding sequences below are predicted from manually evaluated computer analysis, using similarity information and the progra GLIMMER; http://www.tigr.org/softlab/glimmer/glimmer.html and GeneMark; http://opal.biology.gatech.edu/GeneMark/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (29-MAR-2001) Genome Sequencing Center, Department Genetics, Washington University School of Medicine, 4444 Fore Park Boulevard, St. Louis, MO 63108, USA COMMENT Supported by NIH grant 5U 01 AI43283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The Salmonella typhimurium Genome Sequencing Project
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McClelland, M., Sanderson, K.E., Spieth, J., Clifton, S.W.,

McClelland, M., Sanderson, K.E., Spieth, J., Clifton, S.W.,

Latreille, P., Courtney, L., Porwollik, S., Ali, J., Dante, M.,

Hou, S., Layman, D., Leonard, S., Nguyen, C., Scott, K., Holmes, A.,

Grewal, N., Mulvaney, E., Ryan, E., Sun, H., Florea, L., Miller, W.,

Stoneking, T., Nhan, M., Waterston, R. and Wilson, R.K.
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Salmonella typhimurium LT2
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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                                                                                                                                                                                                                                                     Location/Qualifiers
1. .23647
                                                                                                                                              /organism="Salmonella typhimurium LT2"
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complement(110. .5707)
                       /gene="ratA"
/note="synonym: STM2515"
                                                                         complement(110. .5711)
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1 to 23647)
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LFIDAMURKERIODAMUNIKEWASASSEHTUTUVNGOAHLITIKHUSGIG
VETPIRIVADDEGGNEVELSESVITTVUTSDOVDGANNAGHNGVVDAGNLYKRPLLA
VEASHKOGOFSENNEEMATIFNSVASATAGEVOVDGANNAGHNGVVDAGNLYKRPLLA
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KNADAKVGEQVKMNIHSRNALNGMAIGNTDFTITMANGRRRDGLTTGFTDTSNGEMOF
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YSMSENPGNYYLQLCLTTSRSGLNIALSSDAMDAIGASTLKGSTLYWQYKDLKTGNAAG
CODACACUANTITOTVVNOACATATUKOVTTGTGAVAFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="synonym: STM2516" complement(5827. .6786)
/protein_id="AAL21411.1"
                                                                                                                                                                       pestis invasin
                                                                                                                                                                                                                                                                                                 complement(6844. .9036)
                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="putative RBS for complement(6844. .9042)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TLKTNTTYQVLLWSDKNGNGTYDAGENVTDQYDYRWKFVGTSKIAGTGTGGIVNESWN
DKDLVIPVTNAEAKTAFEGADGGVTVGSDGVQGFGLSIDYKRK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 \translation="MQATVKRRLTKVALALVVAGYCAAPAVAANGNLKSGQWQIVSEQ
TGTIQGTVPWITRAADKTADTDKDHVTVTIDRGDKIYTEDKDKYCGKVTVNWAIG
DTEGDLDTDNTATKATVKWYSFSQNGSDKDLGTGGSSFEIQAADADKIGIKITFRIT
TTGDPAVATELLLKDLSTDAGGGSDDDEIPEGPVVDENVHVVIHEKDSNTNLLKNSGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="putative RBS for complement(5827. .6793)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QPQAGVAVLLTRDYAYSRGAVDKQYIEPGVIGEPVPFTTSPANMMLAPVAPAGTAVAF
NNQNGLSTKWSGFTGDDGKLRFTLTQDKSLGLKTSVTAALANQFDEAASVDAIFTVQT
SPDTPYASYWGHMPDTVQVNGVTLRRPYLKAELSAAPRDTWPFNNEFWGTNYYYQSEH
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ILPDAEQLVQMRHEHSTLETWTGWPVAGDAEYWSSTKNQLSGYHAAVHMNSASVVRAA
DSDTLLVSCYUKAQPAAHPQITLSPQGPYKAQYGESIDLTMTVVDRDTQKPLPYBYME
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                                                                                                                                                                                                                                                                                                                                              /note="synonym: STM2517"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene≖"sinI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(6788. .6793)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="putative outer membrane protein"
/protein_id="AAL21410.1"
/db_xref="GI:16421060"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(5706. .5711)
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TTGQTTCTREKATTSGLGSCRVP"
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pestis invasin proteins; (gi|4583531)"
                                                                                                                                                                                                                                                                 /gene="sinH"
                                                                                                                                                                                                                                                                                                                                                                                                /gene≖"sinH"
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CDS

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Alignment
Pred. No.:
                                             Percent Similarity:
Best Local Similarity:
Query Match:
US-09-921-992-78 (1-372)
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/note="putative RBS for s
/note="putative RBS for s
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LEYTFVPLYTVGTDYKAGTGDSNDFSVNATVNYQIGFPLAQLDPENVKIQHSLMGSR
TDFVDRNNFIILSYREKDPLDVIMLKADATNEHBECVIEDTPEDAVGLEKCKWTVNA
LINHYKIISASWQAKNNAARFILWFVVKANALTEGNNNSWNLVLPAWVNADTEEDFYNA
LINHYKVRMTLEDEKGNKQNSGVVEITVQQDRKIELIVDNIADTDRSDHSHEASALAD
GEDGVWADLLITDSFGDSTDRNGNELVDDAMFPVLYDSNDKKYTLAQTPCTFTPCVF
JASRDKEAGTVTLSTLDFFFFWKKAKDAPGDSNYDVTFIGDLSALNAVITCYVKAA
NPVNLIGKEDKHPTVNNAYRFILWRDKKNGGVPGMSBGLTTEEBMALVDYQWEETGQST
NGHTGALANTMNEDLVLPVTNKEAAQKFAANVEDGVQGYGIRVTYSQK"

COMPLEMENT (9037. .9042)
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LGVRQNVGNWLLGGNAFYDYDFTRGHRRLGLGTEAWTDYLKFSGNYYHPLSDWKDSED
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/note="putative RBS for engA;
complement(11283. .12471)
/gene="yfgL"
/note="synonym: STM2520"
                                                                                                                                                                                                                                                                                                                     /product="putative GTP-binding protein"
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/product="putative GTP-binding protein"
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TNRILGEERVVYDMFGTTRDSIYIFMERDEREYVLLDTAGVEKRGKITDAVEKFSVI
KTLQAIEDANVVLLVIDAREGISDQDLSLLGFTLNSGRSLVIVNKNOGLSEVKENV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="yfgJ"
/note="putative RBS for yfgJ;
complement(9692. .11176)
/gene="engA"
/gene="engA"
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/note-"similar to E. coli orf, hypothetical protein
(AAC/75563.1); Blastp hit to AAC/75563.1 (83 aa), 63%
identity in aa 13 - 83"
                                                                                                                                                                                                                                                   TPIRIOFKEGENPYANKRNTLTPTQMRKRKRLMKHIKKSK"
complement(11171. .11176)
                                                                                                                                                                                                                                                                                       KETLDFRLGF IDFARVHF I SALHGSGVGNLFESVREAYDSSTRRVSTAMLTRIMTMAV
EDHQPPLVRGRRVKLKYAHAGGYNPP I VVI HGNQVKDLPDSYKRYLMNV FRKSLEVMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="similar to E. coli putative GTP-binding factor (AAC75564.1); Blastp hit to AAC75564.1 (503 aa), 97% identity in aa 14 - 503"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(9692. .11164)
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                   ThrGlyGlyAsnLysLysSerGlyLeuTyrGluAspGlyValArgLysAspArgLeuAsp 340
                                                                                                                                                         SerIleIleGlyCysValValAsnGlyProGlyGluAlaLeuValSerThrLeuGlyVal
                                                                                                                                                                                                                         ATCGGCACGGTGAACGCGCTGGAGCAGCGTCTGGAAGATATCATCACCCCGATGGACGTC
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                                                                                                                                                                                                                                                                                            CGCGCGCGCGATCAATTTCATCGCCTGCCCGACCTGTTCTCGCCAGGAGTTCGACGTT
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                          Sgo
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                                                                                                                                                                                                                                             RBS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Parkhill, J., Dougan, G., James, K.D., Thomson, N.R., Pickard, D., Wain, J., Churcher, C., Mungall, K.L., Bentley, S.D., Holden, M.T.G., Sebalhia, M., Baker, S., Basham, D., Brooks, K., Chillingworth, T., Connerton, P., Cronin, A., Davis, P., Davies, R.M., Dowd, L., White, N., Farrar, J., Feltwell, T., Hamlin, N., Haque, A., Hien, T.T., Holroyd, S., Jagels, K., Krogh, A., Larsen, T.S., Leather, S., Moule, S., O'Gaora, P., Parry, C., Quail, M., Rutherford, K., Simmonds, M., Skelton, J., Stevens, K., Whitehead, S. and Barrell, B.G. Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18
Nature 413 (6858), 848-852 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (25-OCT-2001) Submitted on behalf of the Salmonalla sequencing team, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salmonella enterica subsp. enterica serovar Typhi Salmonella enterica subsp. enterica serovar Typhi Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AL627275
AL62775
AL62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (URL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E-mail: parkhill@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 145050)
Parkhill, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 413 (6858),
21534947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Details of S. typhi sequencing at the on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11677608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAAGCGCGTCGGATTGACGTGCTGCAGGTTGAAAAA 14494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 145050)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http:,
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                                                                                           /gene="STY2721"
                                                                                                                                                            note-"possible
                                                                                                                                                                                                   /gene="STY2720"
                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="conserved hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="STY2720"
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                                                                                                                                                                                                                                                                                                                                                                                                                         'db_xref+"GI:16503699"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="STY2720"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:90370"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="CT18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ∕organism="Salmonella enterica subsp. enterica serovar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
                                                                                                                                                                                                                                                                            GFSESRYQQFFDEV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     //www.sanger.ac.uk/Projects/S_typhi/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'synonym: yffB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              possible RBS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      coli yffB (YFFB_ECOLI); Fasta hit
81% identity in 118 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sanger Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 are available
                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene
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/gene="STY2723"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    signature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'gene≖"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ignature 2"
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SYPSRERWPPATGEPQPEQAAILSRLREWPPGYATVIAPRGRCKSALAGOFISOMAGT
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LREQALNDEDWRELVGFAFAHRPLLTSLGCLHRLLQYSALPLPALRGRLEEKASDAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Orthologue of E. coli YPFI_ECOLI; Fasta hit to YPFI_ECOLI (671 aa), 72% identity in 662 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(2389. .4404)
/gene="STY2723"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(2389. .4404)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HRDFNDKWDDEDDWPKKDQPKK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="putative membrane
/protein_id="CAD02684.1"
/db_xref="GI:16503701"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="STY2723"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Similar to Escherichia coli similar to TR:P77259
(EMBL:D90875) (66 aa) fasta scores: E(): 1e-27, 95.5% id
in 66 aa. Contains hydrophobic, possible membrane-spanning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptidase family
                                                                                                                                                                                                                                                                                                                                                                                                                                                       transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="MDWLAKYWWILVLVFLVGVLLNVIKDLKRIDHKKFLANKPELPP/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="STY2721"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'db_xref="SPTREMBL:Q8XF02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="PS00759 ArgE / dapE / ACY1 / CPG2 / yscS family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'gene="STY2721"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="PS00758 ArgE /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="STY2721"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Pfam match to entry PF01546 Peptidase_M20,
Peptidase family M20/M25/M40, score 315.30, E-val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="STY2721"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AQVVELGPVNATIHKINECVNAADLQLLARMYQRIMEQLVA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="succinyl-diaminopimelate desuccinylase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dapE / ACY1 / CPG2 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         yscs family
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60

64445

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100

64325

64145

220 64025 200 64085

63905 240 63965

63725 300 63785

320

280 63845 260

63665

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360

63545

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Best Local Si
Query Match:
DB:
                                                                                 Score:
Percent Similarity:
Post Local Similarity:
            δã
                                       US-09-921-992-78 (1-372) x AL627275 (1-145050)
                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene
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                                                                                                                                                                                          gene
                                                                                                                                                                                                                     RBS
                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                       No.:
MetHisAsnGlnAlaProIleGlnArgArgLysSerThrArgIleTyrValGlyAsnVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Pfam match
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complement(4420. .5283)
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/gene-"STY2724"
/note-"Orthologue of E. coli p76563; Fasta hit to E
/note-"Orthologue of E. coli p76563; Contains
(287 aa), 92% identity in 286 aa overlap. Contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(3790. .3813)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(5586...5612)
/gene="STY2725"
/note="PS01058 SAICAR synthetase signature complement(5829...5873)
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/note="PS01057 SAICAR synthetase signature
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/note="possible RBS"
complement(6303...7337)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QQGYLEAGDLEEALNAAQAIGDDRLQQQGQGRVVPDSFTHGTSEQRYSWFKRGFDSGD
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1831.00
99.19%
98.12%
98.12%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 possible membrane-spanning region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to entry PF00583 Acetyltransf, (GNAT) family, score 32.50, E-
                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                 E-value 1
                                                                     4000
                                                                                                                                                                                                                                                                                                                 9 SAICAR_synt,
1.2e-120"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hit to P76563
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η overlap"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProIleGlyAspGlyAlaProIleAlaValGlnSerMetThrAsnThrArgThrThrAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AlaMetArgHisValAspHisLeuAspArgLeuAsnPheAspGlnPheLysValSerVal 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ValProLeuValAlaAspIleHisPheAspTyrArgIleAlaLeuLysValAlaGluTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTGGTGGACTGCGCGCGACAAAAACATCCCTATCCGTATCGGCGTAAATGCCGGATCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LysAlaSerAspValPheLeuAlaValGluSerTyrArgLeuLeuAlaLysGlnIleAsp
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gene	gene CDS	. gene	KEFWORDS SOURCE SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS TITLE JOURNAL FEATURES SOURCE	RESULT 15 AE016835 LOCUS DEFINITION ACCESSION VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="yfiE"
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                                                                  CAGCCGCTGCATCTGGGGATCACCGAAGCGGGCGGCGCGCGTAGCGGGGCGGTTAAGTCG
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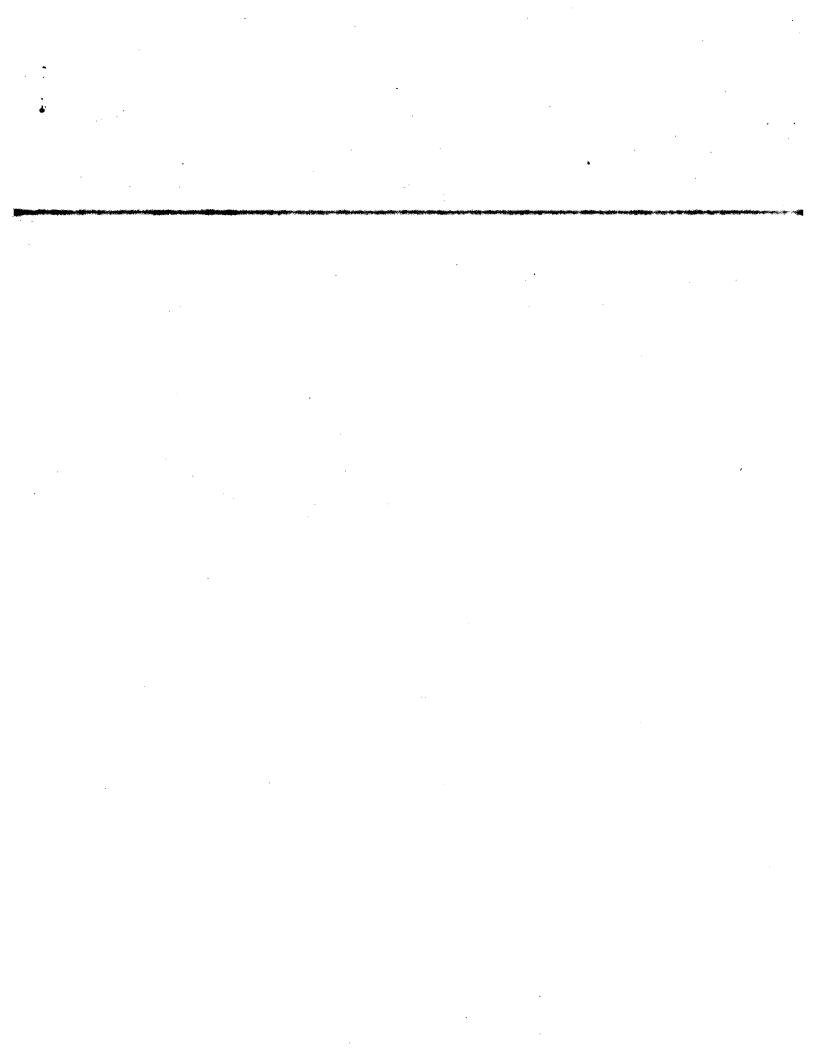
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Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Pred. No. greater is the number of results predicted by chance to have a tear than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

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Escherichia coli.	M. tuberculosis; antibiotic; ds.	H. influenza; S. pneumoniae; H. pvlori; B. burgdorferi; nesticate.	b1808; yeah; yaqF; b1983; yidD; yceG; yibC; antibacterial commoned.	Y99J; YjeE; YiaO; YrdC; YhbC; YqbP; YbeY; gcpE; kdtR; ffs ycat;	Bacterial growth; inhibitor; vqbB; vfhC; vacE; vchB; vafD; vrfT;	E. coli essential gene gcpE.		27-FEB-2001 (first entry)		AAA95478;		AAA95478 standard; DNA: 1119 BP.	RESULT 1 AAA95478

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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to antagonists and inhibitors of 24 bacterial genes and proteins. The proteins are thought to be essential for growth in several species of bacteria (including S. pneumoniae, B. burgdorferi, H. influenza and H. pylori). The proteins and coding sequences shown in the specification can be used to identify antagonists and inhibitors which can be used in disease treatment and pesticides. In particular, they can be used against M. tuberculosis. The present sequence is one of the genes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying antibacterial compounds, comprises identifying an antagonist or inhibitor of the expression of a gene encoding polypeptide essential for bacterial growth or survival claim 1; Fig 1; 75pp; English.
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AAA88705 standard; DNA; 1119
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screening;
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Not given;
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LeuGluLysAspLeuGlnGluLysTyrGlyGluProThrProGlnAlaLeuLeuGluSer
                                   GlyValAspCysLeuArgIleAsnProGlyAsnIleGlyAsnGluGluArgIleArgMet
                                                                                                                                GGCGTCGATTGTCTGCGTATTAACCCTGGCAATATCGGTAATGAAGAGCGTATTCGCATG
                                                                                                                                                                                                                                Page 25;
                                                                                                                                                                                                                                                                                                                                                                                  (1-372) x AAA88705
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is 1 of 22 E. coli genes (see
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                                                                          21-MAY-1999;
21-MAY-1999;
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                                                                                                                                 20-MAY-2000;
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                                                                                                                                                                                                                                                                                    Isoprenoid; gcpE; yfgB; antimicrobial;
antimycotic; antiparasitic; antiviral;
                                                                                                                                                                                                                                                                                                                                               E. coli gcpE
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                                                                      99DE-1023567.
99DE-1023568
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Alignment : Pred. No.: Score:
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes almovel method for incorporating gcpE and yfgB cg genes into viruses and cells for increasing isoprenoid content and identifying e.g. antimicrobial agents, comprises using DNA sequences (1) cfrom the gcpE or yfgB genes of bacteria or parasites or DNA sequences (2) cill which hybridize to the specified genes or encode a plastid protein cwith the same biological activity as those encoded by the genes. The invention also describes (1) plant cells containing (1) or (11); (2) plant cells containing (1) or (11); (2) created containing the enzymatic activity of a cgpE protein; or (4) screening compounds (A) that have antimycotic, antiparasitic, fungicidal or herbicidal activity in humans or animals or antiviral containing the enzymatic activity in plants. (1) and (11) care used: (1) to increase (the isoprenoid levels in viruses and cells; cotential antibacterial, antimycotic, antiparasitic, or antiviral agents or antiviral agents or antiviral agents or animals or antiviral agents or or animals or antiviral agents or or animals or antiviral agents or or animals or animals; or animals, or antiparasitic, fungicidal cor herbicidal agents for agriculture.
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            LeuGluLysAspLeu(
                                               GTGGTTGACTGTGCG
                                                                                                        GlyValAspCysLeuArgIleAsnProGlyAsnIleGlyAsnGluGluArgIleArgMet
                                                                                                                                             GTGCCGCTGGTGGCT
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genes into viruses and cells, for
nt and identifying e.g. antimicrobial
sequences from bacteria or parasites
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Matches:
Conservative:
Mismatches:
Indels:
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RESULT 4
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ID AAD3
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1119
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phosphate pathway, encoding a fully defined GCPE protein which is
useful for increasing levels of tocopherol substrates in plants .
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A genomic DNA of cockroach-symbiotic
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                                                                                                              07-APR-2000; 2000JP-0107160
                                                                                                                                                                                                 Buchnera
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Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a gene (I) derived from Buchnera sp. CC containing the DNA (a) or (b), (a) has a fully defined base pair CC sequence selected from a table of sequences found in the Buchnera sp. CC genomic DNA of ABA92787 given in the specification or is a DNA selected CC from complementary DNA sequences, and (b) is a DNA which hybridises with CC the DNA (a) and encodes a protein. Also described are: (I) a recombinant CC vector (II) containing (I); (2) a transformant (III) containing (I); (3) a genomic DNA of Buchnera sp. containing the sequence given in CC ABA92787; (4) a plasmid derived from Buchnera sp. containing DNA (c) or CC (d), (c) is a DNA containing a fully defined sequence given in ABA92788 CC method for the preparation of a protein in which (III) is cultured and CC the expression protein of the objective protein is collected from the CC resultant culture. The DNA is useful for developing agricultural CC chemicals for exterminating cockroaches. The present sequence represents the specifically claimed Buchnera sp. genomic DNA sequence, from the
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{\tt AspGlnProLeuHisLeuGlyIleThrGluAlaGlyGlyAlaArgSerGlyAlaValLys}
                                 ValLysAlaSerAspValPheLeuAlaValGluSerTyrArgLeuLeuAlaLysGlnIle
                                                                                              TCAGCTATGAGGCATATTGAATACTTTGATGCTTTAAATTTTAATCAATTTAAAGTTAGT
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                                                       Genomic library for identifying diagnostic and therapeutic compositions, and for identifying virulence factors, regulatory elements and drug targets, comprises Moraxella catarrhalis nucl
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The present invention relates to a Moraxella catarrhalis comprising of a combination of 41 nucleic acid molecules

genomic library

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The present invention relates to nucleic acid sequences (ABQ67188-ABQ71212) from Listeria sp. The sequences are useful as probes and primers for identification and/or detection of Listeria (e.g. as contaminants in foods, or mutational analysis) and for analysis of gene expression. Proteins encoded by the nucleic acid sequences can be used to screen for compounds that modulate gene expression, replication and pathogenicity of Listeria (potential therapeutic agents), also for treating infections by Listeria, and are useful as immunogens in
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          Note: The sequence data for this patent did not form of the printed specification, but was obtained in eledirectly from WIPO at ftp.wipo.int/pub/published_pct.
                                                                                                                                                                    Claim 16;
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                                                                                                                      GlyProGlyGluAlaLeuValSerThrLeuGlyValThrGlyGlyAsnLysLysSerGly
                                                                                                                                                                                                                                                                       AlaCysProThrCysSerArgGlnGluPheAspValIleGlyThrValAsnAlaLeuGlu
                                                                                                                                                                                                                                                                                                                                                                      SerGluGlyIleGlyAspThrLeuArgValSerLeuAlaAlaAspProValGluGluIle
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 GluAlaArgIleArgAlaLysAlaSerGlnLeuAspGluAlaArgArgIleAspValGln
                                  CTTTTTAGACATGGTAAAATTATTCGAAAAGTACCGGAAGCTATTATGATAGACGAACTT
                                                                LeuTyrGluAspGlyValArgLysAspArgLeuAspAsnAsnAspMetIleAspGlnLeu
                                                                                                     GGCCCTGGAGAAGCTCGCGAAGCCGATATCGGAATTGCTGGTTCAAACGGAGAAGGCCTT
                                                                                                                                                                     AATTACATAGCAAAGATTGAAGTTCCGATTAAAGTAGCCGTGCTTGGCTGTGCGGTCAAC
                                                                                                                                                                                                     GlnArgLeuGluAspIleIleThrProMetAspValSerIleIleGlyCysValValAsn
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Percent Similarity: Best Local Similarity:

9.72e-76 868.00 67.68% 49.17%

Conservative: Mismatches:

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RESULT 10
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Alignment
                                                                                                                                                                                        The present sequence is the genome sequence of Listeria monocytogenes EGD-e. This sequence and fragments of this sequence are useful for selecting probes and primers for detecting genes in L. monocytogenes are related organisms, and to study genetic polymorphisms and other genome proteins (ABB47297-ABB50149) expressed from the present sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, and for biosynthesis and biodegradation, especially biosynthesis of Vitamin B12. This sequence proteins encoded by it are also useful for selecting compounds that
                                                                                                                                                                                                                                                                                                                                                                                               Genomic sequence for Listeria monocytogenes, useful e.g. for and prevention of Listeria and related bacterial infections,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chakraborty T, Domann E,
Perez-Diaz J, Baquero F,
Maduenio E, De Pablos B,
Rose M, Voss H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200177335-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Listeria monocytogenes
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                                                                                                                          regulate gene expression and cell replication and modulate L. monocytogenes-related diseases. In addition, this sequence and proteins encoded by it are useful in pharmaceutical and vaccines compositions to the treatment or prevention of infections by L. monocytogenes and relate
                                                                                                                                                                                                                                                                                                                                                     Claim 1;
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                               BP; 914202 A;
                                                                                data for this patent did not was obtained in electronic for
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                                                                                                                        AATTACATAGCAAAGATTGAAGTTCCGATTAAAGTAGCCGTGCTTGGCTGTGCGGTCAAC
                                                                                GlyProGlyGluAlaLeuValSerThrLeuGlyValThrGlyGlyAsnLysLysSerGly
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                                                                                                                                                                                                                                                                                                            CTTTTTAGACATGGTAAAATTATTCGAAAAGTACCGGAAGCTATTATGATAGACGAACTT
                            LeuTyrGluAspGlyValArgLysAspArgLeuAspAsnAsnAspMetIleAspGlnLeu
                                                             GGCCCTGGAGAAGCTCGCGAAAGCCGATATCGGAATTGCTGGTTCAAACGGAGAAGGCCTT
                                                                                                                                                    GlnArgLeuGluAspIleIleThrProMetAspValSerIleIleGlyCysValValAsn 308
                                                                                                                                                                                    TCCTGCCCTACTTGCGGTCGAATAGAGATTGATTTAATTCGTATCGCTAATGAAGTGGAA
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                                                                                                                             Sequence 6157
                                                                                                                                                    of the printed specification, directly from WIPO at ftp.wip.
                                                                                                                                                                                      The present invention relates to nucleic acid sequences (ABQ67188-ABQ71212) from Listeria sp. The sequences are useful as probes and primers for identification and/or detection of Listeria (e.g. as contaminants in foods, or mutational analysis) and for analysis of gene expression. Proteins encoded by the nucleic acid sequences can be used to screen for compounds that modulate gene expression, replication and pathogenicity of Listeria (potential therapeutic agents), also for treating infections by Listeria, and are useful as immunogens in anti-Listeria vaccines.
                                                                                                                                                                                                                                                                                                                      Claim 14;
                                                                                                                                                          inti-Listeria vaccines.
Note: The sequence data for this patent did not form part
Note: The sequence data for this patent did not form part
                                                                                                                                                                                                                                                                                                                                              antibodies and modulators
                                                                                                                                                                                                                                                                                                                                                        New genomic sequences from Listeria sp
treatment and prevention of infection,
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(1-372)

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Query

Match:

Percent Similarity:
Best Local Similarity:

Conservative: Mismatches:

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cc The invention describes a method of monitoring differential expression of cc genes in a first Bacillus cell relative to expression of the genes in cother Bacillus cells, comprising hybridising labelled nucleic acid probes isolated from Bacillus cells to a substrate containing array of Bacillus cells to a substrate containing array of Bacillus cells relative gene expression by an observed hybridisation reporter signal of cc relative gene expression by an observed hybridisation reporter signal of cc genes in a first Bacillus cell relative to expression of the same genes cc in one or more second Bacillus cells. The method is useful for monitoring close everal genes from a Bacillus cell, discovering new cc genes, identifying possible functions of unknown open reading frames and contitoring gene copy number variation and stability. Monitoring changes cc in expression of genes may be used to provide a representation of the way contitoring changes in culture conditions, cells adapt to changes in culture conditions.

Cc environmental stress or other physiological provocation. Extensive contitoring changes are suppressed to the provide a representation of the same copy number variation and stability. Monitoring changes compared to the provide a representation of the way continue to the physiological provocation. Extensive continues are continued to the provide and array continued to the provide and the provide and array continued to the provide and the
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                                                       (first entry)
                                                                                                     DNA;
 detection;
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Novel polynucleotide comprising Bifidobacterium genome sequence useful as a probe or primer for detecting and/or identifying Bifidobacterium longum in a biological sample -
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                                                                                                                                                                                                                                                                30-JAN-2001; 2001EP-0102050
                                                                                                                                                                                                                                                                                                      Bifidobacterium
                                                                                                                                                                                                                                                                                                                   identification;
rotavirus; food
                                                                                                                                                                                                                                                                                                              lactic acid bacterium; diarrhoea; pathogenic bacteria; composition; pharmaceutical composition; gene; ds.
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Claim 1; SEQ ID 1; 80pp; English.

The present invention describes a polynucleotide (I) comprising a CC sequence of a Bifidobacterium genome selected from the nucleotide CC sequences given in AB081842 and AB081843, or a sequence exhibiting at CC least 90% identity or which hybridises with the sequences given in CC AB081842 and AB081843. Also described is a polynucleotide (II) encoding a fusion protein, comprising a sequence selected from 1097 sequences given in AB081843. Also described is a polynucleotide (II) encoding cC given in AB081843. Also described is a polynucleotide (II) encoding a heterologous polypeptide. (I) has antidiarrheic and cencoding a heterologous polypeptide. (I) has antidiarrheic and composition of Bifidobacterium longum in a biological sample. A carrier containing cC (I) (which is a probe) is useful for the detection and/or identification cf Bifidobacterium longum in a biological sample. A carrier containing cc pathogenic bacteria and/or treating diarrhea brought about by pathogenic bacteria and/or rotavirus. The carrier is a food composition containing N.B. The sequence data for specification but is based European Patent Office. this patent on sequence is not represented in the printed information supplied by the

Sequence B₽; 72540 Α, 102738 C; 103221 G; 71481 Ţ, 0

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Best Local Similarity:
                                                                                                         US-09-921-992-78 (1-372) x ABQ81842
                                                                                                                                       Query Match:
                                                                                                                                                                    Score:
                                                                                                                                                                                     Alignment
                                                                                                                                                                            No.:
                                                                       118761
                42
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                            GluAlaThrValAsnGlnIleLysAlaLeuGluArgValGlyAlaAspIleValArgVal
                                                                  AGCGAATCGCCCTTGCACCCGCGCCCCCAAGTCCCGCCGCATCATGGTGGGTCCGGTGCCG
                                                                          AsnGlnAlaProIleGln---ArgArgLysSerThrArgIleTyrValGlyAsnValPro
                                                                                                                            1.95e-71
814.50
65.65%
46.26%
43.65%
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ABQ67188-ABQ71212) from Listeria sp. The sequences are useful as probe and primers for identification and/or detection of Listeria (e.g. as contaminants in foods, or mutational analysis) and for analysis of gene expression. Proteins encoded by the nucleic acid sequences can be used to screen for compounds that modulate gene expression, replication and pathogenicity of Listeria (potential therapeutic agents), also for treating infections by Listeria, and are useful as immunogens in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (INSP )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           anti-Listeria vaccines.
Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic for the printed specification int/pub/published_pct_sequences directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 14; SEQ ID 1137; 180pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibodies and modulators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New genomic sequences from Listeria species, useful treatment and prevention of infection, also related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antibacterial; Listeria; infection; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the present invention relates to nucleic acid sequences (ABQ67188-ABQ71212) from Listeria sp. The sequences are
                                                                                                                                                                                                                                                                                                                                                                                                                       No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2002-332479/37
                                                                                                                                                                                                                                                                                                                                                                                                                                  Scores:
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                                                                                                                               GCCAATGCTCTTAGTGCCATCAAGAAAAGGATTCATATTCCTCTTGTGGCAGATATTCAT
                                                                                                                                                                                         CACCGATTAGAAGAGGTGGGTTGTCAGATTGTGCGAGTTGCTTGTCCTGATGAGCGTGCA
                                                                                                                                                                                                                                                    GCTGGAAAGAGCATGACTACAAAGCTACATGATGTCGAAGCAACAGTAGCGGAAATT
                                                                                                                                                                                                                                                                       AlaValGlnSerMetThrAsnThrAsqThrThrAspValGluAlaThrValAsnGlnIle
                               ProGlyAsnIleGlyAsnGluGluArgIleArgMetValValAspCysAlaArgAspLys
                                                                                     PheAspTyrArgIleAlaLeuLysValAlaGluTyrGlyValAspCysLeuArgIleAsn 108
                                                                                                                                                        AlaGluAlaPheLysLeuIleLysGlnGlnValAsnValProLeuValAlaAspIleHis
           CCTGGTAACATCGGTCGCCGTGATCGGGTGGAAAAAGTGGTTAATGCTGCTAAAGCAAAA
                                                                                                                                                                                                                      Lys \texttt{AlaLeuGluArgValGlyAlaAspIleValArgValSerValProThrMetAspAla}
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                                                                     TTTGATTACCGACTAGCACTTAAAGCTATTGATGCAGGTGTTGACAAAATCCGGATTAAT
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812.00
70.32%
52.90%
43.52%
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                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
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used to develop of Helicobacter

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Tomb Ģ

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other;

1180 162 73 73 117 2

208 596 536

128 419

359 108 302 88 68

242

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122

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AAX14017
YAX AAX14
XX AAX14
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XX GHPO
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01-APR-1997;
24-JUN-1997;
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                                                         01-APR-1998;
                                                                                                  W09843478-A1
                                                                                                                                                                                       GHPO protein; Helicobacter peptic ulcer disease; ss.
                                                                                                                                                                   Helicobacter
                                                                                                                                                                                                                       H. pylori
                                                                                                                                                                                                                                             31-MAR-1999
                                                                                                                                                                                                                                                                   AAX14017;
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GAAGATTTAGATTTTATGATATCATTGTTTCTTTGAAAGCTTCTGATGTGAATTTAGCA
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97US-0833457.
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                                                       98WO-US06371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a polynucleotide of the invention. It was isolated from Helicobacter pylori and encodes a H.pylori GHPO protein. The polypeptides can be used for preventing or treating Helicobacter infections, and gastroduodenal diseases associated with these infections, including acute, chronic, and atrophic gastritis, and peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also be used for the production of antibodies. The products can also be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1180 BP; 380 A; 206
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                                 AspArgLeuAsnPheAspGlnPheLysValSerValLysAlaSerAspValPheLeuAla
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                     TyrGlyGluProThrProGlnAlaLeuLeuGluSerAlaMetArgHisValAspHisLeu
                                                                                                                                                    CCCGGAAACATCGGCTCTAAAGAGAAGATCAAAGCGGTGGTTGATGCTTGTAAAGAAAAA
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1076	ATCATTAAAGAGGGTAAAGTCATTCACAAACTGGCTGAAAAGGATTTATTT	1017	뮹
348	LeuTyrGluAspGlyValArgLysAspArgLeuAspAsnAsnAspMetIleAspGlnLeu 348	329	VΩ
1016	957 GCTTTGGGTGAAGCCAAGCATGCAGACATGGCGATCGCTTTTGGGAATCGCAGCGGTTTG 1016	957	뮹
328	309 GlyProGlyGluAlaLeuValSerThrLeuGlyValThrGlyGlyAsnLysLysSerGly 328	. 309	Qy
956	AAACGCTTAAGCCACATCAAAACCCCCTTTAGACATTAGCGTGATGGGTTGCGTGGAAT	897	Ъ
308	GlnArgLeuGluAspIleIleThrProMetAspValSerIleIleGlyCysValValAsn	289	Qy
896	TCTTGCCCCACTTGCGGGCGCATTGAAGCCAATTTAGTGGATATGGCGATCAAGGTAGAA	837	В
288	269 AlaCysProThrCysSerArgGlnGluPheAspValIleGlyThrValAsnAlaLeuGlu 288	269	VΩ
836	AAAGTGGCCAGAGCAATTTTTACGCCATAGCGGGCGGTTGAAAGAAGGGATTAATTGGATT	777	
268	LysValGlyPheAspIleLeuLysSerLeuArgIleArgSerArgGlyIleAsnPheIle	249	ΩУ
776	ATGGAGGCATTGGGGATACGATGCGCGTATCCATCACAGGGGAATTAGAAAATGAAATC	717	뮹
248	229 SerGluGlyIleGlyAspThrLeuArgValSerLeuAlaAlaAspProValGluGluIle 248	229	Ωy
716	GAGGCGGGAATCTTTTTAGCTCCAGTATCAAATCCGCTATGGCTTTTAGGGGGGGCTTTTA	657	Ъ
228	209 GluAlaGlyGlyAlaArgSerGlyAlaValLysSerAlaIleGlyLeuGlyLeuLeuLeu 228	209	ρy
656	::: ::: ::: aragaagcttacaggatgcttcgccctcttgtgatctatcctttccatttgggggttacg 656	597	B

Search completed: August 15, 2003, 01:38:42 . Job time : 3223 secs

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-LOOPEXT=0 -UNITS=blts -START=1 -END=-1 -MATRIX-blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LOGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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1: /cgn2_6/ptodata/
2: /cgn2_6/ptodata/
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Sequence 6420, Ap
Sequence 6131, Ap
Sequence 6339, Ap
Sequence 10, Appli
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## 10 Sequence Seq							
1353 72.5 886 4 US-09-170-187-10 812 43.5 886 2 US-08-827-190-9 812 43.5 886 4 US-09-281-991A-6251 812 43.5 886 4 US-09-170-187-9 812 43.5 886 4 US-09-291A-6251 85 15.5 1083 4 US-09-291A-6269 8470.5 25.2 1230025 4 US-09-282-991A-12534 8470.5 25.2 1230025 4 US-09-282-991A-12534 811.5 6.0 3377 4 US-09-282-991A-12534 811.1 5.9 1665 4 US-09-282-991A-12534 811.1 5.9 1665 4 US-09-282-991A-1267 81.1 5.9 1665 4 US-09-282-991A-1267 81.1 5.9 1665 4 US-09-282-991A-1267 82.1 106.5 5.7 1854 4 US-09-282-991A-1267 83.6 5.7 2259 4 US-09-282-991A-1267 83.6 5.7 2129 3 US-09-291A-1267 83.6 5.7 2129 3 US-09-291A-1267 83.6 5.7 2129 4 US-09-136-421B-1 84.1 101.5 5.4 2989 1 US-08-453-523-1 85.4 1694 3 US-09-282-991A-12816 85.4 1363 4 US-09-282-991A-12816 85.4 1363 4 US-09-328-52-3604 85.4 11601 2 US-08-222-617A-24 85.4 11601 2 US-08-222-617A-24	Seque	US-09-252-991	3414	υ	99.5	45	•••
1353 72.5 886 4 US-09-170-187-10 812 43.5 886 2 US-08-827-190-9 812 43.5 886 2 US-08-827-190-9 812 43.5 886 4 US-09-252-918-6251 82 40.3 4403765 3 US-09-103-840A-2 751.5 40.3 441529 3 US-09-103-840A-1 607.5 25.2 1230025 4 US-09-252-991A-6269 470.5 25.2 1230025 4 US-09-252-991A-12534 111.5 6.0 3978 4 US-09-252-991A-12534 111.5 6.0 3998 3 US-09-066-046-5 111.5 5 1083 4 US-09-252-991A-1267 106.5 5.7 1854 4 US-09-252-991A-1267 106.5 5.7 2259 4 US-09-252-991A-1267 106.5 5.7 2129 3 US-08-252-991A-1267 105.5 5.7 2129 3 US-08-975-762-39 105.5 5.7 2129 3 US-08-975-762-39 105.5 5.7 2129 3 US-08-975-762-39 105.5 5.7 2129 3 US-09-252-991A-1267 101.5 5.4 2989 1 US-08-442-3-3-1 101.5 5.4 2989 1 US-08-440-520-1 101.5 5.4 2989 1 US-08-453-323-1 101.5 5.4 2989 1 US-08-91A-13125 101.5 5.4 2989 1 US-09-252-991A-13125 101.5 5.4 2989 1 US-09-252-991A-13125 101.5 5.4 2989 1 US-09-328-352-3604 100.5 5.4 11601 2 US-09-328-352-3604 100.5 5.4 11601 2 US-09-222-617A-3	Seque	US-08-222-617A-2	11601	5.4	100.5	44	٠,
1353 72.5 886 4 US-09-170-187-10 812 43.5 886 2 US-08-827-190-9 812 43.5 886 2 US-08-827-190-9 812 43.5 886 2 US-08-827-190-9 812 43.5 886 2 US-09-120-187-9 812 43.5 886 2 US-09-120-187-9 813 43.5 886 2 US-09-120-187-9 814 43.5 886 2 US-09-120-187-9 815 40.3 4403765 3 US-09-123-840A-2 816 54 3 411529 3 US-09-123-840A-2 817 51.5 40.3 441529 3 US-09-123-10178-209 817 52.5 21230025 4 US-09-252-991A-12534 818 5 15.5 1083 4 US-09-252-991A-14259 818 5 15.9 166.5 4 US-09-252-991A-14267 818 5 15.9 166.5 4 US-09-252-991A-14267 819 5 166.9 1854 4 US-09-252-991A-14267 810 5.7 1664976 4 US-09-252-991A-784 810 5.7 1664976 4 US-09-252-991A-784 811 10.5 5.7 2129 3 US-08-916-582-39 810 5.5 2214 1 US-09-916-582-39 810 5.4 1694 3 US-09-125-991A-13125 811 5.4 2989 1 US-08-453-23-1 81 101 5.4 1398 4 US-09-252-991A-13125 81 101 5.4 1398 4 US-09-252-991A-13125 81 100 5 5.4 1693 4 US-09-252-991A-13125 81 100 5 5.4 1693 4 US-09-252-991A-13125 81 100 5 5.4 1693 4 US-09-252-991A-13125 81 100 5 5.4 1398 4 US-09-252-991A-13125 81 100 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	Seque	US-08-222-617	11601	5.4	100.5	43	G
1353 72.5 886 4 US-09-170-187-10 812 43.5 886 2 US-08-827-190-9 812 43.5 886 4 US-09-170-187-9 812 43.5 886 4 US-09-170-187-9 812 43.5 886 4 US-09-170-187-9 812 43.5 886 2 US-08-827-190-9 812 43.5 886 4 US-09-120-187-9 812 43.5 886 2 US-09-120-187-6251 S 813.4 43.5 886 4 US-09-120-187-6251 S 815.5 183 4 US-09-120-1918-6209 S 8470.5 32.6 543 4 US-09-221-0178-309 8470.5 32.6 543 4 US-09-221-0178-309 8111.5 6.0 3998 3 US-09-066-046-55 8111.5 9 1665 4 US-09-221-0178-1017 8111.5 5.7 164976 4 US-09-252-991A-14267 S 8111.5 5.7 2129 3 US-09-252-991A-184 812.5 1.5 1694 3 US-09-136-4218-1 813.5 5.7 2129 4 US-09-136-4218-1 813.5 5.4 2989 1 US-08-440-520-1 814.5 14.6 14.6 14.0 15.0 15.4 11.4 15.0 15.0 15.4 11.4 15.0 15.0 15.4 11.4 15.0 15.0 15.4 11.4 15.0 15.0 15.4 11.4 15.0 15.0 15.0 15.4 11.4 15.0 15.0 15.0 15.4 11.4 15.0 15.0 15.0 15.0 15.0 15.0 15.0 15.0	Seque	US-09-039-859-	2010	•	100.5	42	
1353 72.5 886 4 US-09-170-187-10 812 43.5 886 2 US-08-827-190-9 812 43.5 886 2 US-08-170-187-9 812 43.5 886 2 US-09-170-187-9 812 43.5 886 2 US-09-170-187-9 812 43.5 886 2 US-09-170-187-9 813 40.3 4403765 3 US-09-103-840A-1 8470.5 25.2 1230025 4 US-09-123-840A-1 8470.5 25.2 1230025 4 US-09-123-1017B-309 8111.5 6.0 3177 4 US-09-221-017B-309 8111.5 6.0 3998 3 US-09-066-046-5 8111.5 6.0 3998 3 US-09-066-046-5 8111.5 5.7 2129 4 US-09-221-017B-1017 8106.5 5.7 243 4 US-09-252-991A-14350 8105.5 5.7 2429 4 US-09-252-991A-14350 8105.5 5.7 2429 3 US-08-916-421B-1 8105.5 5.7 2429 3 US-08-915-6421B-1 8101.5 5.4 2989 1 US-08-446-313-1 8101.5 5.4 2989 1 US-08-445-323-1 8101.5 5.4 2989 1 US-08-440-520-1 8101 5.4 1398 4 US-09-252-991A-13125 8101.5 5.4 2989 1 US-08-440-520-1 8101 5.4 1398 4 US-09-252-991A-13125 8101.5 5.4 2989 1 US-08-440-520-1 8101 5.4 1398 4 US-09-252-991A-13125 8101.5 5.4 2989 1 US-08-440-520-1 8101 5.4 1398 4 US-09-252-991A-13125 8101.5 5.4 2989 1 US-08-440-520-1 8101 5.4 1398 4 US-09-252-991A-13125 8101.5 5.4 2989 1 US-08-440-520-1 8101 5.4 1398 4 US-09-252-991A-13125 8101.5 5.4 2989 1 US-08-440-520-1 8101 5.4 1398 4 US-09-252-991A-13125 8101.5 5.4 2989 1 US-08-440-520-1 8101 5.4 1398 4 US-09-252-991A-13125 8101.5 5.4 2989 1 US-08-440-520-1 8101 5.4 1398 4 US-09-252-991A-13125 8101.5 5.4 2989 1 US-08-440-520-1 8101 5.4 1572 4 US-09-612-964-1	Seque	US-09-328-352-36	1863	•	100.5	41	
1353 72.5 886 4 US-09-170-187-10 812 43.5 886 2 US-08-827-190-9 S 812 43.5 886 2 US-09-123-190-6251 S 812 43.5 886 2 US-09-123-840A-2 84.0 9 555 4 US-09-123-840A-2 85.1 40.3 441352 3 US-09-123-991A-6209 S 85.2 1230025 4 US-09-125-991A-12534 S 85.1 10.8 4 US-09-225-991A-12534 S 85.1 10.8 5 10.8 4 US-09-225-991A-14257 S 85.1 10.8 5 10.8 4 US-09-252-991A-14267 S 85.1 10.8 5 10.8 4 US-09-252-991A-181 S 85.1 10.8 5 10.8 4 US-09-252-991A-181 S 85.1 10.8 5 10.8 4 US-09-252-991A-13125 S 85.1 10.8 5 10.8 4 US-09-252-991A-13125 S 85.1 10.8 5 10.8 4 US-09-252-991A-13125 S	Seque	US-09-612-964-	1572	•	101	40	
1353 72.5 886 4 US-09-170-187-10 S 812 43.5 886 2 US-08-827-190-9 S 812 43.5 886 4 US-09-328-3980 S 812 43.5 886 4 US-09-170-187-9 S 813 40.3 4403765 3 US-09-103-840A-1 8607.5 32.6 543 4 US-09-291A-6269 S 8470.5 55.2 1230025 4 US-09-282-991A-12534 S 8111.5 6.0 3998 3 US-09-06-046-55 S 8111.5 6.0 3998 3 US-09-06-046-55 S 8111.5 9 1665 4 US-09-282-991A-12534 S 8111.5 5.7 1854 4 US-09-282-991A-14350 S 8111.6 5.7 1854 4 US-09-282-991A-14350 S 8111.6 5.7 164976 4 US-09-282-991A-14350 S 8105.5 5.7 2129 3 US-09-106-582-39 S 8105.5 5.7 2129 3 US-09-106-582-39 S 8105.5 5.7 2129 4 US-09-136-421B-1 S 8105.5 5.4 2989 1 US-08-440-520-1 S 8105.5 5.4 2989 1 US-08-440-520-1 S 8105.5 5.4 1149 4 US-09-252-991A-13125 S	Seque	US-09-252-991A-12	1398	5.4	101	9	
1353 72.5 886 4 US-09-170-187-10 812 43.5 886 2 US-08-827-190-9 S 812 43.5 886 2 US-09-170-187-9 S 813 43.5 886 2 US-09-170-187-9 S 814 43.5 886 2 US-09-170-187-9 S 815 40.3 4403765 3 US-09-103-840A-1 8470.5 25.2 1230025 4 US-09-128-452A-1 8470.5 25.2 1230025 4 US-09-221-0178-309 8111.5 6.0 397 4 US-09-221-0178-309 8111.5 6.0 397 4 US-09-221-0178-1017 8111.5 6.0 397 4 US-09-251-0178-1017 8111.5 6.0 3998 3 US-09-066-046-5 8111.5 5.7 1854 4 US-09-252-991A-14267 S 8111.5 5.7 2259 4 US-09-252-991A-14267 S 8111.5 5.7 166497 4 US-09-252-991A-14267 S 8111.5 5.7 2129 3 US-08-975-762-39 812.5 5.7 2129 3 US-08-975-762-39 813.5 5.5 2214 1 US-09-136-421-11 S 8111.5 5.4 2989 1 US-08-443-323-1 S 8111.5 5.4 2989 1 US-08-440-220-1 S	Sequer	US-09-252-991A-13	1149	5.4	101	88	C
1353 72.5 886 4 US-09-170-187-10 S 812 43.5 886 2 US-08-827-190-9 S 812 43.5 886 2 US-09-170-187-9 S 812 43.5 886 2 US-09-170-187-9 S 812 43.5 886 2 US-09-170-187-6251 S 812 40.3 4403765 3 US-09-103-840A-2 8470.5 25.2 1230025 4 US-09-123-840A-2 8470.5 25.2 1230025 4 US-09-128-452A-1 848.5 15.5 1083 4 US-09-251-91R-12534 S 848.5 15.5 1083 4 US-09-251-91R-12534 S 849.5 15.5 1084 4 US-09-251-91R-14350 S 849.5 15.5 1854 4 US-09-252-991R-14350 S 849.5 15.5 1854 4 US-09-252-991R-14350 S 849.5 15.5 164976 4 US-09-252-991R-14267 S 849.5 15.5 164976 4 US-09-252-991R-14267 S 849.5 105.5 5.7 2129 3 US-09-916-582-39 S 849.5 105.5 5.7 2129 3 US-08-975-762-39 S 849.5 105.5 5.7 2129 4 US-09-105-582-39 S 849.5 105.5 5.7 2129 4 US-09-105-582-39 S 849.5 105.5 5.4 2989 1 US-07-985-458-1 S 859.5 105.5 5.4 2989 1 US-08-453-123-1 S	Sequer	US-08-440-520-	2989	5.4	101.5	37	
1353 72.5 886 4 US-09-170-187-10 S 812 43.5 886 2 US-08-827-190-9 S 812 43.5 886 4 US-09-281-991A-6251 S 812 43.5 886 4 US-09-170-187-9 S 813 44.3 4403765 3 US-09-103-840A-1 S 8470.5 25.2 1230025 4 US-09-198-452A-1 S 8470.5 25.2 1230025 4 US-09-281-017B-399 S 8470.5 25.2 1230025 4 US-09-281-017B-399 S 8470.5 25.2 1230025 4 US-09-281-017B-399 S 8470.5 25.2 1230025 4 US-09-281-017B-1017 S 8470.5 25.7 1083 4 US-09-281-017B-1017 S 8470.5 25.7 1854 4 US-09-281-017B-1017 S 8470.5 25.7 1854 4 US-09-281-91A-14267 S 8470.5 25.7 1664976 4 US-09-281-91A-14267 S 8470.5 5.7 1664976 4 US-09-281-91A-784 S 8470.5 5.7 2129 3 US-09-291A-784 S 8470.5 5.7 2129 3 US-09-106-882-39 S 8470.5 5.7 2129 4 US-09-106-882-39 S 8470.5 5.4 1694 3 US-09-136-421-11 S 8470.5 5.4 2989 1 US-07-927-851-1	Sequen	08-453-323-	2989	5.4	101.5	36	
1353 72.5 886 4 US-09-170-187-10 S 812 43.5 886 2 US-08-827-190-9 S 812 43.5 886 2 US-08-827-190-9 S 812 43.5 886 4 US-09-170-187-9 S 812 43.5 886 4 US-09-170-187-9 S 812 43.5 886 4 US-09-170-187-9 S 813 40.5 886 4 US-09-170-187-9 S 814 40.5 886 4 US-09-170-187-9 S 815 40.3 4403765 3 US-09-103-840A-1 S 816 5 15.5 1083 4 US-09-1291A-6209 S 817 52.5 21230025 4 US-09-221-017B-309 S 817 55 6.0 3998 3 US-09-221-017B-309 S 811 5.9 1665 4 US-09-221-017B-1017 S 811 5.9 1665 4 US-09-221-017B-1017 S 816 5.7 16649 4 US-09-252-991A-14350 S 817 106 5.7 2259 4 US-09-252-991A-14350 S 817 106 5.7 166496 4 US-09-252-991A-14350 S 818 5 1.7 166497 4 US-09-252-991A-14350 S 819 5 5.7 2129 3 US-08-975-762-39 S 810 5.5 2214 1 US-09-295-028-39 S 810 5.5 2214 1 US-09-136-421-11 S	Sequen	07-927-851-	2989	5.4	101.5	35	
1353 72.5 886 4 US-09-170-187-10 S 812 43.5 886 2 US-08-827-190-9 S 812 43.5 886 2 US-08-120-187-9 S 812 43.5 886 2 US-09-170-187-9 S 812 43.5 886 2 US-09-170-187-9 S 812 43.5 886 2 US-09-170-187-9 S 812 43.5 86 3 US-09-170-8040-2 S 812 5 12.3075 3 US-09-103-840A-2 S 812 5 15.5 1083 4 US-09-251-91A-12534 S 813 5 15.5 1083 4 US-09-252-91A-12534 S 813 5 15.5 1083 4 US-09-252-91A-14350 S 814 5 15.5 1083 4 US-09-252-91A-14350 S 815 5 7 164976 4 US-09-252-991A-14367 S 816 5 7 164976 4 US-09-252-991A-14367 S 817 106 5 7 1664976 4 US-09-252-991A-784 S 818 7 105 5 7 1664976 4 US-09-16-812-39 S 819 5 5 7 2129 3 US-08-916-782-39 S 819 5 5 7 2129 4 US-09-106-582-39 S 810 5 5 7 2129 4 US-09-106-582-39 S	Sequen	09-136-421-	1694	5.4	101.5	34	
1353 72.5 886 4 US-09-170-187-10 S 812 43.5 886 2 US-08-827-190-9 S 812 43.5 886 4 US-09-282-991A-6251 S 751.5 40.3 4401529 3 US-09-103-840A-2 751.5 40.3 4411529 3 US-09-103-840A-2 751.5 40.3 4411529 3 US-09-103-840A-1 607.5 32.6 54.3 4 US-09-128-491A-6209 S 470.5 32.6 54.3 4 US-09-282-991A-12534 S 111.5 6.0 3998 3 US-09-282-991A-12534 S 111.5 6.0 3977 4 US-09-282-991A-12534 S 111.5 9 1665 4 US-09-282-991A-12534 S 111.6 5 7 1854 4 US-09-282-991A-14350 S 116.5 5.7 1854 4 US-09-252-991A-14350 S 106.5 5.7 2259 4 US-09-252-991A-14367 S 106.5 5.7 2259 4 US-09-252-991A-784 S 105.5 5.7 2129 3 US-09-916-421B-1 S 105.5 5.7 2129 3 US-09-916-421B-1 S 105.5 5.7 2129 4 US-09-250-393 S	Sequen	07-985-458-	2214	5 5	103.5	<u>ω</u>	
1353 72.5 886 4 US-09-170-187-10 812 43.5 886 2 US-08-827-190-9 812 43.5 886 4 US-09-328-352-3780 S 812 43.5 886 4 US-09-170-187-9 8751.5 40.3 4403765 3 US-09-103-840A-1 8751.5 40.3 4411529 3 US-09-103-840A-1 8761.5 32.6 54 4 US-09-221-017B-309 8761.5 55 1083 4 US-09-221-017B-309 8761.5 50.0 3377 4 US-09-221-017B-309 8761.5 50.0 3377 4 US-09-221-017B-1017 8761.5 50.0 3378 4 US-09-221-017B-1017 8761.5 50.0 3378 4 US-09-252-991A-14350 8761.5 50.0 368 4 U	Sequen	09-106-582-	2129	5.7	105.5	32	•
1353 72.5 886 4 US-09-170-187-10 S 1195 64.0 1137 4 US-09-328-352-3780 S 812 43.5 886 2 US-08-827-190-9 S 812 43.5 886 2 US-08-827-190-9 S 812 43.5 886 2 US-08-827-190-9 S 812 43.5 886 2 US-09-170-187-9 S 812 43.5 886 2 US-09-170-187-187 S 812 43.5 140.3765 3 US-09-170-187-187 S 812 52.5 1230025 4 US-09-178-178-187 S 812 52.5 1230025 4 US-09-252-991A-12534 S 813 53 16.5 1083 4 US-09-252-991A-14350 S 814 55.7 1854 4 US-09-252-991A-14350 S 815 5.7 2943 4 US-09-252-991A-14367 S 816 5.7 1664976 4 US-09-252-991A-14367 S 816 5.7 1664976 4 US-09-18-291A-1881 S 816 5.7 1664976 4 US-09-18-19-18-18-18-18-18-18-18-18-18-18-18-18-18-	Sequen	9-295-028-	2129	5.7	105.5	31	a
1353 72.5 886 4 US-09-170-187-10 S 812 43.5 886 2 US-08-827-190-9 S 812 43.5 886 4 US-09-28-291A-6251 S 812 43.5 886 4 US-09-170-187-9 S 812 43.5 886 4 US-09-170-187-9 S 812 43.5 886 4 US-09-170-187-9 S 813 44.5 886 4 US-09-170-187-9 S 814 43.5 886 4 US-09-170-187-9 S 815 40.3 440555 4 US-09-252-991A-6251 S 816 54 40.5 99.103-840A-2 US-09-103-840A-2 S 817 51.5 1083 4 US-09-252-991A-6209 S 818.5 15.5 1083 4 US-09-221-017B-309 S 819 51.5 1083 4 US-09-221-017B-107 S 8111.5 6.0 3998 3 US-09-06-046-5 S 8111.5 9 1665 4 US-09-221-017B-1017 S 8111.5 9 1665 4 US-09-221-017B-1017 S 8111.5 9 1665 4 US-09-252-991A-14367 S 8111.5 9 1665 4 US-09-252-991A-14367 S 811.5 106.5 5.7 1854 4 US-09-252-991A-14367 S 811.5 106.5 5.7 1854 4 US-09-252-991A-14367 S 811.5 106.5 5.7 1854 4 US-09-252-991A-14367 S 811.5 106.5 5.7 1664976 4 US-08-916-421B-1	Œ	8-975-762-	2129	5.7	105.5	30	••
1353 72.5 886 4 US-09-170-187-10 S 1195 64.0 1137 4 US-09-328-352-3780 S 812 43.5 886 2 US-08-827-190-9 S 812 43.5 886 4 US-09-170-187-9 S 812 43.5 886 4 US-09-170-187-9 S 812 43.5 886 4 US-09-170-187-9 S 813 43.5 886 4 US-09-170-187-9 S 814 43.5 886 4 US-09-170-187-9 S 815 40.3 4403765 3 US-09-103-840A-1 8607.5 32.6 543 4 US-09-2991A-6209 S 8470.5 32.6 543 4 US-09-221-017B-309 S 8470.5 32.6 1330025 4 US-09-221-017B-309 S 8111.5 6.0 398 3 US-09-066-046-5 S 8111.5 6.0 3998 3 US-09-066-046-5 S 8111.5 5.7 1854 4 US-09-252-991A-14350 S 8110.5 5.7 2943 4 US-09-252-991A-14350 S 8110.5 5.7 2943 4 US-09-252-991A-14350 S 8110.5 5.7 2943 4 US-09-252-991A-14350 S	Seque	US-08-916-421B-	6497	5.7	106	29	• •
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1353 72.5 886 4 US-09-170-187-10 S 1812 43.5 886 2 US-08-827-190-9 S 812 43.5 886 4 US-09-28-291A-6251 S 751.5 40.3 4403765 3 US-09-103-840A-2 751.5 40.3 4411529 3 US-09-103-840A-2 751.5 40.3 4411529 3 US-09-103-840A-1 101.5 5.7 1854 4 US-09-252-991A-6209 S 112.5 6.0 3177 4 US-09-252-991A-12534 S 111.5 5.0 3998 3 US-09-260-066-5 S 111 5.9 1665 4 US-09-221-017B-1017 S 1106.5 5.7 1854 4 US-09-252-991A-12534 S	Sequen	9-252-991A-	2943	5.7	106.5	27	
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ALIGNMENTS

Sequence 8 Patent No. CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CATTOIL, Peter G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: CASE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410 TELEFAX: (415) 397-8338 INFORMATION FOR SEQ ID NO: 8: GENERAL INFORMATION: COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS SEQUENCE CHARACTERISTICS: SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA: APPLICANT: Rather, TITLE OF INVENTION: TITLE OF INVENTION: CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES: LENGTH: TYPE: n FILING DATE: APPLICATION NUMBER: COUNTRY: CITY: San Francisco ADDRESSEE: 8, Application US/08827190 5. 5858367 94104 California 220 Montgomery United Medlen & Carroll, base pairs States Philip N.
Methods For (
Utilizing aa Release #1.0, Version #1.30 US/08/827,190 of America Street, CASE-02443 LLP et, Suite or Screening For Antimicrobials aarC And Compositions Thereof

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AlaAlaAspProValGluGluIleLysValGlyPheAspIleLeuLysSerLeuArgIle
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                                CGTTCGCGAGGGATCAACTTCATCGCCTGCCCGACCTGTTCGCGTCAGGAATTTGATGTT
                                           GCGGCCGATCCGGTCGAAGAGATCAAAGTCGGTTTCGATATTTTGAAATCGCTGCGTATC
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Query Match:
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Patent No. 6383745
GENERAL INFORMATION:
APPLICANT: Rather, Philip N.
TITLE OF INVENTION: Methods For
TITLE OF INVENTION: Utilizing as
                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (415) 397-833
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEVEN.

CORRESPONDENCE ADDRESS:

ANDRESSEE: Medlen & Carroll, LLP

ANDRESSEE: Medlen & Carroll, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: CA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Peter G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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COUNTRY:
ZIP: 941
                                                                                                                                                                                                                                                                                                                                            LENGTH: 1010 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
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OPERATING SYSTEM:
SOFTWARE: Patenti
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CITY: San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE:
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                                                                                                               MetHisAsnGlnAlaProIleGlnArgArgLysSerThrArgIleTyrValGlyAsnVal
                                CCGATTGGCGATGGTGCTCCCATCGCCGTACAGTCCATGACCAATACGCGTACGACAGAC
                                                  ProIleGlyAspGlyAlaProIleAlaValGlnSerMetThrAsnThrArgThrThrAsp
                                                                                               ATGCATAACCAGGCTCCAATTCAACGTAGAAAATCAACACGTATTTACGTTGGGAATGTG
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Methods For Screening For Antimicrobial
Utilizing aarC And Compositions Thereof
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Sequence 4, Application US/08827190; Patent No. 5858367; GENERAL INFORMATION: APPLICANT: Rather, Philip N. TITLE OF INVENTION: Methods For Scr. TITLE OF INVENTION: Utilizing marc ANUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS: ADDRESSE: Medlen & Carroll, LLP STREET: 220 Montgomery Street, S. CITY: San Francisco
STATE: California
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US-08-827-190-4
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REFERENCE/DOCKET NUMBER: CASE
TELECOMMUNICATION INFORMATION:
TELEPAN: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
1.F.NUGTH. 13:5'---
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ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/827,190
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NAME/KEY: CDS
LOCATION: 175..1272
OTHER INFORMATION: //
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ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Peter G.
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TYPE: nucleic acid
STRANDEDNESS: double
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US-09-170-187-4
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Patent No. 6383745
GENERAL INFORMATION:
APPLICATION NUMBER: US
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 01
FILING DATE:
                                                                                                                                                NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
andressee: Medlen & Carroll, LLP
                                                                                                                                                                                     APPLICANT: Rather, TITLE OF INVENTION: TITLE OF INVENTION:
                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                        SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                      ADDRESSEE: Medlen & Carr
STREET: 220 Montgomery S
CITY: San Francisco
STATE: California
COUNTRY: United States o
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Methods For Screening For Antimicrobials
Utilizing aarC And Compositions Thereof
                                                                 Release #1.0, Version
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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REGISTRATION NUMBER: 32.837
REFERENCE/DOCKET NUMBER: CA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   No.:
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LOCATION: 175..1272
OTHER INFORMATION: /
OTHER INFORMATION: /
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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                                                                                                                                             ATGCATAATGAATCACCGATAAAAAGACGTAAATCCACCCGAATTTATGTAGGTAACGTG
    GlnProLeuHisLeuGlyIleThrGluAlaGlyGlyAlaArgSerGlyAlaValLysSer
                                LeuGluLysAspLeuGlnGluLysTyrGlyGluProThrProGlnAlaLeuLeuGluSer 160
                                                                                                          DNA (genomic)
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RESULT 5
US-09-557-884-1
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PATENT NO. 6506581

GENERAL INFORMATION:

APPLICANT: Fleischmann et al.

APPLICANT: The Nucleotide sequence of the Hamman of the Hamman the Hamman the Hamman and Hamman Hamman
                                       INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                               COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Deall Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION NUMBER: US/09/557,884
FILING DATE: 25-Apr-2000
FILING DATE: 25-Apr-2000
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION NUMBER: 08/476,102
FILING DATE: JUN-5-1995
ATTORNEY/AGENT INFORMATION:
NAME: MICHELE S. MAIKS
REGISTRATION NUMBER: 41,971
PREFERENCY FOOVER
                                                                             TELEFAX: 301-309-8439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Scients STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1135
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| CAATTGGTCTTGGTATGTTGGCTGAAGGTATCGGCGATACGTTACGTATCTCACTC
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Query Match:
DB:
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STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ
US-09-557-884-1
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                                            LeuGlyLeuLeuLeuSerGluGlyIleGlyAspThrLeuArgValSerLeuAlaAlaAsp
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Alignment Scores: 1.38e-2570 Length: 1830121 Pred. No.: 1603.50 Matches: 320 Score: 3.6	; SEQUENCE DESCRIPTION: SEQ ID NO: 1: US-09-643-990A-1	SEQUENCE CHARACTERISTICS: LENGTH: 1830121 base pairs TYPE: nucleic acid STRANDEDNESS: double	FELECOMMUNICATION INFORMATION: FELEPHONE: 301-500-5790 FELEPAX: 310-309-8439 INFORMATION FOR SEQ ID NO. 11:	ATTORNEY/AGENT INFORMATION: NAME: Kenley K. HÖOVER REGISTRATION NUMBER: 40,302 REFERENCE/DOCKET NUMBER: PB186P1C1	APPLICATION NUMBER: 08/48/,429 ; FILING DATE: 1995/06-07 ; APPLICATION NUMBER: 08/426,787 ; FILING DATE: 1995/04-21	APPLICATION NUMBER: US/09/643,990A FILING DATE: 23 Aug-2000 CLASSIFICATION: CURKnown> PRIOR APPLICATION DATA: PRIOR APPLICATION DATA:			ADDRESSE: Human Genome Sciences, inc. STREET: 9410 Key West Avenue CITY: Rockville, STATE: MD	he Haemophilus introduced in the Haemophilus introduced in the Haemophilus introduced in the Haemophilus interest in the Haemophilus	sequence of	6528289 NFORMATION: ICANT: Robe Mark	RESULT 6 US-09-643-990A-1 ; Sequence 1, Application US/09643990A	Qy 363 ArgArgIle 365 Db 392052 AACAGAATT 392060	Qy 343 AspMetIleAspGlnLeuGluAlaArgIleArgAlaLysAlaSerGlnLeuAspGluAla 362	Qy 324 ASDLYSSETGLYL <mark>eu</mark> TyrGluASpGlYValArgLysASpArgLeuASpAsnAsn 342 	Db 391812 GTARATGCGCTAGAACARCGCCTTGAAGATATTACTACCAATGGATGTATCTATTACC 391871 Oy 304 GlyCysValValAsnollyProGlyGluAlaLeuValSerThrLeuGlyValThrGlyGly 323 Lillillillillillillillillillillillillill
Qy 324 AsnLysLysSerGlyLeuTyrGluAspGlyValArgLysAspArgLeuAspAsnAsn 342 	Qy 304 GlyCysValValAsnGlyProGlyGluAlaLeuValSerThrLeuGlyValThrGlyGly 323	ω ω	Oy 264 GlyIleAsnPheIleAlaCysProThrCysSerArgGlnGluPheAspVallleGlyThr 283	Qy 244 ProValGluGluIleLysValGlyPheAspIleLeuLysSerLeuArgIleArgSerArg 263	OY 224 LeuGlyLeuLeuSerGluGlyIleGlyAspThrLeuArgValSerLeuAlaAlaAsp 243 ::: :::	Qy 204 HisLeuGlyIleThrGluAlaGlyGlyAlaArgSerGlyAlaValLysSerAlaIleGly 223	Qy 184 AspValPheLeuAlaValGluSerTyrArgLeuLeuAlaLysGlnILeAspGlnProLeu 203	Qy 164 HisValAspHisLeuAspArgLeuAsnPheAspGlnPheLysValSerValLysAlaSer 183	OY 144 ASPLEUGINGIULYSTYTGIYGIUPTOThrPrOGInAlaLeuLeuGluSerAlaMetArg 163 	Qy 124 CysalaargasplysasnileProIleArgIleGlyValasnalaGlySerLeuGluLys 143 	QY 104 CYSLeuArgIleAsnProGlyAsnIleGlyAsnGluGluArgIleArgMetValValAsp 123	QY 84 ValalaAspīleHisPheAspTyrArgīleAlaLeuLysValaIaGluTyrGlyValAsp 103 	Qy 64 ProThrMetAspAlaAlaGluAlaPheLysLeuIleLysGlnGlnValAsnValProLeu 83	Qy 44 ThrValAsnGlnIleLysAlaLeuGluArgValGlyAlaAspIleValArgValSerVal 63	Qy 24 AspGlyAlaProIleAlaValGlnSerMetThrAspThrArgThrThrAspValGluAla 43	Qy 4 GlnAlaProIleGlnArgArgLysSerThrArgIleTyrValGlyAsnValProIleGly 23	Percent Similarity: 93.66% Conservative: 20 Best Local Similarity: 88.15% Mismatches: 22 Query Match: 85.93% Indels: 1 DB: 4 Gaps: 1 US-09-921-992-78 (1-372) x US-09-643-990A-1 (1-1830121)

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Best Local Similari
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US-08-827-190-7
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INFORMATION FOR SEQ ID NO: "SEQUENCE CHARACTERISTICS:
LENGTH: 1079 base pairs
TYPE: nucleic acid
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REFERENCE/DOCKET NUMBER: CA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
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ATTORNEY/AGENT INFORMATION:
NAME: CATTOll, Peter G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                              GlnIleLysAlaLeuGluArgValGlyAlaAspIleValArgValSerValProThrMet
                                                               CCTATTGCCGTGCAATCAATGACAAATACTCGCACCACTGATGTGGAAGCGACAGTTGCT
                                                                              ProIleAlaValGlnSerMetThrAsnThrArgThrThrAspValGluAlaThrValAsn
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Methods For Screening For Antimicrobials
Utilizing marC And Compositions Thereof
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Matches:
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                                             Sequence 7, Application US/09170187
Patent No. 6383745
GENERAL INFORMATION:
APPLICANT: Rather, Philip N.
TITLE OF INVENTION: Methods For S.
TITLE OF INVENTION: Utilizing dar
NUMBER OF SEQUENCES: 13
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                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, SI
CITY: San Francisco
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INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1079 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/170,187
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REFERENCE/DOCKET NUMBER: CA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
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ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Peter G.
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Matches:
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                      US-09-921-992-78 (1-372) x US-09-252-991A-6420 (1-1644)
                                                            Best Local Similarity:
Query Match:
                                                                                                                                                     ; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-6420
                                                                                                    SCOLE
                                                                                                                             Alignment Scores:
                                                                                       Percent Similarity:
                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 6420
LENGTH: 1644
                                                                                                                                                                                                                                                                                                                                                                     Sequence 6420, Application Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                  FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
CURRENT FILING NUMBER: US 60/074,788
                                                                                                                                                                                                                                                                                                  APPLICANT: MARC J. Rubenfleid et al. AMINO ACID TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS A FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1998-0
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-18
PRIOR PELING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 6.331
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
TYPE: TN: 2202
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GENERAL INFORMATION:
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                                                                                                                      ValValAspCysAlaArgAspLysAsnIleProIleArgIleGlyValAsnAlaGlySer 140
                                                            GCCATGCGCCACGTCGATCATCTCGACAAGCTGGACTTCCAGAACTTCAAGGTCAGCGTC
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gTGCCGCTGGTCGCCGACATCCACTTCGACTATCGCATCGCCCTGCGCGTCGCCGAGCTG 182
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                                                                    US-09-921-992-78
                                                                                                                     Query Match:
                                                                                                                                                                                   Pred.
                                                                                                                                                                                                  Alignment Scores
                                                                                                                                                                                                                                 ; ORGANISM: Pseudomonas
US-09-252-991A-6339
                                                                                                                                                                                                                                                                                                                            APPLICANT: MARC J. Rubenfield ITITLE OF INVENTION: AEROGINO FILE REFERENCE: 107196.136 CURRENT APPLICATION NUMBER: 020 CURRENT FILING DATE: 1999-02 PRIOR APPLICATION NUMBER: US PRIOR APPLICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6339, Applic Patent No. 6551795 GENERAL INFORMATION: APPLICANT: Marc J.
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SEQ ID NO 6339
LENGTH: 2088
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FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CATTOLL, Peter G.
REGISTRATION NUMBER: 32,83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (415) 397-8338 INFORMATION FOR SEQ ID NO: 1 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: CA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll,
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TYPE: nucleic acid
STRANDEDNESS: double
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CITY: San Francisco
STATE: California
COUNTRY: United States of Ameri
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                                                                      AsnileProileArgileGlyValAsnAlaGlySerLeuGluLysAspLeuGlnGluLys:148
                                                                                                                                                              LysAlaLeuGluArgValGlyAlaAspIleValArgValScrValProThrMctAspAla
  TACGGTGAGCCAACACCTGAAGCATTGGTTGAATCAGCAATGCGACATGTTGATATCTTG
                     TyrGlyGluProThrProGlnAlaLeuLeuGluSerAlaMetArgHisValAspHisLeu
                                                                                                           CCAGGTAATATCGGCAGTGAAGAGCGTATTCGCCAAGTCGTTGATAGTGCTCGTCATCAC
                                                                                                                           ProGlyAsnIleGlyAsnGluGluArgIleArgMetValValAspCysAlaArgAspLys
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INVENTION: Methods For Screening For Antimicrobials
INVENTION: Utilizing aarC And Compositions Thereof
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                        TELEFAX: (415) 397-833
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 886 base pairs
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APPLICANT: Rather
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TITLE OF INVENTION: Meti
TITLE OF INVENTION: Util
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                             REFERENCE/DOCKET NUMBER: CF.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Peter G.
REGISTRATION NUMBER: 32,837
                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE:
                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Medlen & Carroll, L. STREET: 220 Montgomery Street, CITY: San Francisco STATE: California
TYPE: nuclei
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GENERAL INFORMATION:
APPLICANT: GATY L. BROTON et al.
APPLICANT: GATY L. BUCLEIC ACID AND AMINO ACID SEC
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND T
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID 00 3780
LENGTH: 1137
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; TYPE: DNA
; ORGANISM: Acinetobacter
US-09-328-352-3780
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Sequence 9, Application US/08827190 Patent No. 5858367
                                                                                                                              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAITCH!, Peter G.
REGISTRATION NUMBER: 32,837
REGERENCE/DOCKET NUMBER: CASE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPAX: (415) 397-8338
TUCCHARTIN EDS SEN IN NO. 0.
              LENGTH: 886 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomi
08-827-190-9
                                                                                                                       TELEPHONE: (415) 705-
TELEFAX: (415) 397-83
INFORMATION FOR SEQ ID NO:
                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 886 base pairs
                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Rel
                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Medlen & Carroll, LLP
                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 220 Montgomery Street,
CITY: San Francisco
STATE: California
COUNTR: United States of Ameri
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ValValAsnGlyProGlyGluAlaLeuValSerThrLeuGlyValThrGlyGlyAsnLys 325
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                                                                                                                                                                                                                                                                                                                                                                                                          United States of America
                          DNA (genomic)
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Methods For Screening For Antimicrobials
Utilizing aarC And Compositions Thereof
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Query Match:
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                                                                310 ProGlyGluAlaLeuValSerThrLeuGlyValThrGly 322
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                                            CCTGGTGAAGCGAGAAGCTGATATCGGAATCGCCGGC
                                                                                                                                                                   TGCCCGACTTGCGGCCGTATTGAGATTGATCTAATCAGCATTGCCAATGAAGTGGAAGAG
                                                                                                                                                                                                                               GTAGCAAGGGAGCTTCTGAAATCTTTCGGCTTAGCCTCCAATGCTGCCACGCTCATCTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ArgLeuAsnPheAspGlnPheLysValSerValLysAlaSerAspValPheLeuAlaVal 189
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RESULT 15 US-08-827-190-9/c

Sequence

GENERAL INFORMATION: APPLICANT: Rather

FILING DATE:

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Result
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-Q-/cgn2_1/USPTO_spool/US09921992/runat_12082003_094917_17547/app_query.fasta_1.519
-DB=Published_Applications_NA -QrMT=fastap -SUFFIX=rnpb -MINMARCH=0.1
-LOOPCL-0 -LOOPEXT=0 -UNITS-bits -STARFI=1 -END=-1 -MATRIX-blosum62
-TRANS-human40.cdi -LIST-45 -DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE-LOCAL -OUTFMT=pto -NORM-ext -HBAFSIZE-500 -MINLEN=0
-MAXLEN=200000000 -USER=US09921992_eCGN _1_1_233_erunat_12082003_099917_17547
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -MAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELDET=7
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Ygapop 10.0 , Ygapext
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1: /cgn2_6/ptodata/1/pubpna
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             1119 9
             US-09-921-992-3
                                                                                                                                                                    SUMMARIES
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2553.723 Million cell updates/sec
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Sequence 3, Appli
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GENERAL INFORMATION:

APPLICANT: Boronat, Albert;

APPLICANT: Campos, Narciso;

APPLICANT: Rodriguez-Concepcion, Manuel;

APPLICANT: Rodriguez-Concepcion, Manuel;

APPLICANT: Rodriguez-Concepcion, Manuel;

APPLICANT: Valentin, Henry E.;

APPLICANT: Valentin, Henry E.;

APPLICANT: Venkatesh, Mylavarapu

TILE OF INVENTION: Methyl-D-Erythritol Phosphate Pathway Genes

FILE REFERENCE: 16516.107/35-21(51897)US

CURRENT FILING DATE: 2001-08-06

PRIOR APPLICATION NUMBER: US/09/921,992

CURRENT FILING DATE: 2001-08-06

PRIOR FILING DATE: 2001-08-07

NUMBER OF SEQ ID NOS: 85

LENCTH: 1119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-921-992-3
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Patent No. US20020069426A1
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                ORGANISM: Escherichia coli
FEATURE:
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9 US-09-91-992-2
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       IleGlyThrValAsnAlaLeuGluGlnArgLeuGluAspIleIleThrProMetAspVal
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NAME/KEY: misc_feature
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CURRENT APPLICATION NUMBER: US/10/329,960
CURRENT FILING DATE: 2003-01-02
PRIOR APPLICATION NUMBER: US 09/643,990
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: US 08/487,429
PRIOR APPLICATION NUMBER: US 08/487,429
PRIOR APPLICATION NUMBER: US 08/426,787
PRIOR APPLICATION NUMBER: US 08/426,787
PRIOR FILING DATE: 1995-04-21
NUMBER OF SEQ ID NOS: 1
                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/10329960 Publication No. US20030099277A1 GENERAL INFORMATION:
                                                                        SOFTWARE: PatentIn
SEQ ID NO 1
                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Nucleotide Sequence of the TITLE OF INVENTION: Thereof, and Uses Thereof FILE REFERENCE: PB186P1
CURRENT ADDITO: PB186P1
TYPE: DNA ORGANISM: Haemophilus influenzae FEATURE:
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NAME/KEY: m1sc_feature LOCATION: (107248)..(107248) OTHER_INFORMATION: n equals NAME/KEY: misc_feature LOCATION: (105121)..(105121) OTHER INFORMATION: n equals a, PATURE:
NAME/KEY: misc_feature
LOCATION: (102696)..(102696)
OTHER INFORMATION: n equals a, NAME/KEY: misc_feature .OCATION: (80024)..(80024) DTHER_INFORMATION: n equal NAME/KEY: misc_feature OCATION: (100091)..(100091) WIHER INFORMATION: n equals NAME/KEY: misc_feature ...CATION: (65313)...(65313) THER INFORMATION: n equals NAME/KEY: misc_feature OCATION: (65309)..(65309) WHER INFORMATION: n equals NAME/KEY: misc_feature LOCATION: (47036)..(47036) OTHER INFORMATION: n equals a, NAME/KEY: misc_feature OCATION: (51805)...(51805) OCATION: n equal VAME/KEY: m1sc_feature .OCATION: (51334)..(51334) DTHER INFORMATION: n equals a, NAME/KEY: misc_feature LOCATION: (45732)..(45732) OTHER_INFORMATION: n equals NAME/KEY: misc_feature LOCATION: (44975)..(44975) OTHER_INFORMATION: n equals NAME/KEY: misc_feature LOCATION: (44905)...(44905) OTHER_INFORMATION: n equal NAME/KEY: misc_feature LOCATION: (44416)...(44416) OTHER INFORMATION: n equals a, EATURE: EATURE AME/KEY: misc_feature OCATION: (55369)..(55369) THER_INFORMATION: n equals AME/KEY: misc_feature OCATION: (51786)..(51786) THER INFORMATION: n equals THER INFORMATION: n equals NAME/KEY: m1sc_feature .OCATION: (45593)..(45593) DTHER INFORMATION: n equals EATURE EATURE: EATURE: AME/KEY: misc_feature OCATION: (51602)..(51 EATURE: equals equals equals Ð, a, 8 ď, a, a, 8 a, ğ a, 9 a, ŗ Ĺ Ĺ Ĺ Ĺ Ĺ ί, Ĺ ί, Ĺ Ĺ Ĺ Ĺ Ĺ Ĺ Ĺ Ļ Ĺ φ ď g g φ 9 g g g g g g ۵ g φ g or ç 얹 ç ů, ç မ္ပ or P ဝူ or or ဝူ ç or or ç ဝူ O o o C a O a Ω a

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|ACAGTTGCTCAAATTAAATCATTAGAACGTGTTGGTGCAGATATTGTTCGTGTATCTGTT 39:
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                                                         ValProTleGlyAspGlyAlaProTleAlaValGlnSerMetThrAsnThrArgThrThr
                           ArgValSerValProThrMetAspAlaAlaGluAlaPheLysLeuIleLysGlnGlnVal
                                                                                                                      AspValGluAlaThrValAsnGlnIleLysAlaLeuGluArgValGlyAlaAspIleVal 59
    MetValValAspCysAlaArgAspLysAsnIleProIleArgIleGlyValAsnAlaGly
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US-09-921-992-78 (1-372) x US-09-790-988-1 (1-640681)
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CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: JP2000-107160
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09790988 Patent No. US20020127687A1
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: SHIGENOBU, SHUJI
APPLICANT: WATANABE, HIDEMI
APPLICANT: HATTORI, MASAHIRA
APPLICANT: SAKAKI, YOSHIYUKI
TITLE OF INVENTION: GENOME DNA OF
FILE REFERENCE: 081356/0159
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APPLICANT: Berka, Randy M.

APPLICANT: Clausen, Ib Groth

ITILE OF INVENTION: Methods for Monitoring Multiple Gen

ITILE OF INVENTION: Expression

FILE REFERENCE: 10085.500-US

CURRENT APPLICATION NUMBER: US/09/974,300

CURRENT FILING DATE: 2001-10-05

PRIOR APPLICATION NUMBER: 09/680,598

PRIOR APPLICATION NUMBER: 60/279,526

PRIOR FILING DATE: 2001-03-27

NUMBER OF SEQ ID NOS: 8481

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1692
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                                                                                                                                                                                                                                                                                  Sequence 1692, Application Patent No. US20020146721A1 GENERAL INFORMATION:
              ORGANISM: Bacillus licheniformis -09-974-300-1692
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                                            GATTACATCGCGAAAATCAAGGCGCCGATCAAAGTTGCCGTTCTCGGCTGTGCCGTCAAC
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                                                                                                     TCCTGCCCGACTTGCGGCCGGATCGAAATCGATTTGATCTGCATTGCCAATGAATTCGAA
                                                                                                                               AlaCysProThrCysSerArgGlnGluPheAspValIleGlyThrValAsnAlaLeuGlu
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US-10-156-761-2548
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APPLICANT: HATTORI, MASAHIRA

TITLE OF INVENTION: NOVEL POÜTUUCLEOTIDES

FILE REFERENCE: 249-262

CURRENT APPLICATION NUMBER: US/10/156,761

CURRENT FILLING DATE: 2002-05/29

PRIOR APPLICATION NUMBER: JD 2001-204089

PRIOR FILLING DATE: 2001-05/30

PRIOR FILLING DATE: 2001-05/30

PRIOR FILLING DATE: 2001-08-03

PRIOR FILLING DATE: 2001-08-03
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SEQ ID NO 2548
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
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                                                                                                                                                                  SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
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                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASHHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: OMURA, SATOSHI APPLICANT: IKEDA, HARUO
                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
               NAME/KEY: misc_feature LOCATION: (4187715)
                                                                FEATURE:
                                                                                       ORGANISM: Streptomyces avermitilis
                                                                                                                                        LENGTH:
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CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 08/833,457
PRIOR FILING DATE: 1997-04-01
NUMBER OF SEQ ID NOS: 370
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 195
LENGTH: 1180
TYPE: DNA
ORGANISM: Helicobacter pylori
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Tomb, Jean-Francois
APPLICANT: Oomen, Raymond P.
TITLE OF INVENTION: Identification
TITLE OF INVENTION: Encoding No. U
TITLE OF INVENTION: Genome
FILE REFERENCE: 06132/041002
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PheAspTyrArgIleAlaLeuLysValAlaGluTyrGlyValAspCysLeuArgIleAsn
                                                                                                                                                                          AlaValGlnSerMetThrAsnThrArgThrThrAspValGluAlaThrValAsnGlnIle 48
                                        GCTCTAGCCTTAAAAGAATTGAAAAAAAGTGTCCCCTTTGCCTTTAATCGCTGATATTCAT
                                                                AlaGluAlaPheLysLeuIleLysGlnGlnValAsnValProLeuValAlaAspIleHis 88
                                                                                           GACAGACTCAAACTCGCCGGGGCCGATTTAGTGAGGGTGGCGGTGAGTAATGAAAAGGAC
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APPLICANT: ISHIKAWA, JUN

APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHHEA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
TILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-20
PRIOR APPLICATION NUMBER: JP 2001-272697
                                                                                                                                                                                                                 RESULT 8
US-10-156-761-1636
                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                         Sequence 1636, Application Publication No. US200301190
                                                                                                                                     APPLICANT: OMURA, ŚATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
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ORGANISM: Streptomyces avermitilis
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                        CCCGTCGAGGAGATCAAGGTCGGCATCCAGATCCTGGAGTCGCTGGGCCTCAGGCAGCGG
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NOS: 15109
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CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
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SEQ ID NO 2205
LENGTH: 1134
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APPLICANT:
APPLICANT:
APPLICANT:
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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
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TYPE: DNA
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APPLICANT: MIZOGUCHI, HIROSI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
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TATEISHI, NAOKO
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Sequence 1, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
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                                               SOFTWARE: Fast
SEQ ID NO 110
LENGTH: 1164
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APPLICANT: Marcotte, Edward M.
TITLE OF INVENTION: DETERMINING THE FUNCTIONS
TITLE OF INVENTION: INTERACTIONS OF PROTEINS
FILE REFERENCE: 07419-032001
CURRENT APPLICATION NUMBER: US/09/712,363
CURRENT FILING DATE: 2000-11-13
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ORGANISM: Mycobacterium tuberculosis 09-712-363-110
                                                                                                                     PRIOR APPLICATION NUMBER: 60/165,086
PRIOR FILING DATE: 1999-11-12
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PRIOR APPLICATION NUMBER: 60/117,844
PRIOR FILING DATE: 1999-01-29
                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/179,531
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APPLICATION NUMBER: 60/134,092
FILING DATE: 1999-05-14
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FILING DATE: 1999-02-01
                                                                                                                                                             APPLICATION NUMBER: 60/165,124 FILING DATE: 1999-11-12
                                                                                                                                                                                                                                                                       FILING DATE: 1999-03-26
                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/134,093
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AsnGlyProGlyGluAlaLeuValSerThrLeuGlyValThrGlyGlyAsnLysLysSer
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                                                                                GluGlnArgLeuGluAspIleIleThrProMetAspValSerIleIleGlyCysValVal
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DB:
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APPLICANT: Robmer, Michel;
APPLICANT: Seeman, Myriam;
APPLICANT: Seeman, Myriam;
APPLICANT: Valentin, Henry E.;
APPLICANT: Venkatesh, Tyamagondlu V.;
APPLICANT: Venkatesh, Mylavarapu
TITLE OF INVENTION: Methyl-D-Erythritol Phosphate Pat
FILE REFERENCE: 16516.107/35-2151897)US
CURRENT APPLICATION NUMBER: US/09/921,992
CURRENT FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: US 60/223,483
PRIOR APPLICATION DATE: 2000-08-07
NUMBER DE SEO 150.00-08-07
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Best Local Similarity:
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APPLICANT: Campos, Narciso;
APPLICANT: Rodriquez-Concep
APPLICANT: Rohmer, Michel;
APPLICANT: Seeman, Myriam;
APPLICANT: Valentin, Henry
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LENGTH: 2520
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Patent No. US20020069426A1
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LOCATION: (154)..(2376)
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ORGANISM: Arabidopsis thaliana
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     GTTGCAGATATTCATTTTGCCCCTACTGTAGCCTTACGAGTCGCTGAATGC---TTTGAC
                       ValAlaAspIleHisPheAspTyrArgIleAlaLeuLysValAlaGluTyrGlyValAsp 103
                                                                                                                                                                                                            ATGAGAATAGCGGATAAAGGAGCTGATATTGTAAGGATAACTGTTCAAGGGAAGAAGAG
                                                                                                                                                                                                                                 AlaValGlnSerMetThrAsnThrArgThrThrAspValGluAlaThrValAsnGlnIle 48
                                                                                                                                                                                                                                                                            AGAAGGAAGACTCGTACTGTTATGGTTTGGAAATGTCGCCCTTGGAAGCGAACATCCGATA 462
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                                                                         GCGGATGCGTTTGAAATAAAAGATAAACTCGTTCAGCTTAATTACAATATACCGCTG
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                                                                    NAME/KEY: misc_feature; LOCATION: 2, 645, 659; OTHER INFORMATION: n = US-10-066-543-1184
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Percent Similarity:
              Score:
                          Pred. No.:
                                         Alignment Scores:
                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/066,543
CURRENT FILING DATE: 2002-01-31
NUMBER OF SEQ ID NOS: 3417
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1184
LENGTH: 706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                     APPLICANT: Durham, Margarita
APPLICANT: Stolk, John A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: AND DIAGNOSIS OF COLON
FILE REFERENCE: 210121.563
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                                                                                                                               FEATURE:
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Fanger, Gary R.
Smith, Carole L
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                                                                                                                                                    SEQ ID NO 22
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APPLICANT: Campos, Narciso;
APPLICANT: Rodriguez-Concepcion,
                                                                                                                                                           PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 85
                                                                                                                                                                                                        FILE REFERENCE: 16516.107/35-21(51897)US CURRENT APPLICATION NUMBER: US/09/921,992 CURRENT FILING DATE: 2001-08-06
                                                                                                                                                                                                                                                  APPLICANT: Valentin, Henry E.;
APPLICANT: Venkatesh, Tyamagondlu V.;
APPLICANT: Venkatzamesh, Mylavarapu
TITLE OF INVENTION: Methyl-D-Erythricol Phosphate Pathway Genes
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Seeman, Myriam;
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APPLICANT: Campos, Narciso;
APPLICANT: Rodriguez-Concepci
APPLICANT: Rohmer, Michel;
APPLICANT: Seeman, Myriam;
APPLICANT: Valentin, Henry E.
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                              NUMBER OF SEQ ID NOS:
SEQ ID NO 23
LENGTH: 596
                                                                                                                                                                                                                                                                                                                 Sequence 23, Application US/09921992
Patent No. US20020069426A1
                                                                         APPLICANT: Valentin, Henry E.;
APPLICANT: Venkatesh, Tyamagondlu V.;
APPLICANT: Venkatesh, Tyamagondlu V.;
APPLICANT: Venkatramesh, Wilavarrapu
TITLE OF INVENTION: Methyl-D-Erythritol Phosphate Pathway Genes
EILE REFERENCE: 16516.107/35-21(51897)US
CURRENT APPLICATION NUMBER: US/09/921,992
CURRENT APPLICATION NUMBER: US/09/921,992
CURRENT FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: US 60/223,483
PRIOR FILING DATE: 2000-08-07
ORGANISM: Zea mays
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Rohmer, Michel;
Seeman, Myriam;
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US-09-921-992-23
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                                                                erIleIleGlyCysValValAsnGlyProGlyGluAlaLeuValSerThrLeuGlyValT
TGGGT
                      hrGly 322
                                           NCGTCATGTGCTGTATTGTCAATGGCCCCGGTGCAATGGCCGATGCCGACTATGGCTATG
                                                                                         GGAAGACGTGTTACATGAAGTCCGAGATGCCACTAAACATCTAACGTGTTTAGACTTTCG
                                                                                                              uGluGlnArgLeuGluAspIle-------IleThrProMetAsp-Vals 301
                                                                                                                                          TGTGGCCTGTCCTTCCTGTGGCCGCACGTTGTTCAAC---
                                                                                                                                                     eIleAlaCysProThrCysSerArgGlnGluPheAspValIleGlyThrValAsnAlaLe ::::||||||||:::
                                                                                                                                                                                                         ulleLysValGlyPheAspIleLeuLysSerLeuArgIleArgSerArgGlyIleAsnPh
                                                                                                                                                                                                                                         TACCCCCGAGGGCATGGTGCAATCGGCCCTGGAATTCATCAAAATTTGTGAGTCCTTAGA 128
                                                                                                                                                                                          AATTCCCGTTTGCTACAGCATTCTCCAGGCGCTGGGTTTGCGGAAAACCATGGTGGAATA
                                                                                                                                                                                                                                                                                         TCGCCTCATGGTGAAACGTATGGACGACTTGGGCATGGATTATCCCCTCCATCTAGGGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGGATCGGCGTTAACCATGGTTCTCTCTCCGAAAGAATGC-----TTTTACCTACTTTT
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Search completed: August 15, Job time: 27217 secs 2003, 10:15:58

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Result
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                     1831
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1866
1 MHNQAPIQRRKSTRIYVGNV......RAKASQLDEARRIDVQQVEK 372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               283308 seqs, 96168682 residues
                                                                                                                                                                                                                                                                                                                                                                                                           PIR_76:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd
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  DB
ABO822

AG0828

F82283

F82283

F844063

F83171

E84963

H87354

G97121

A83825

AI1254

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C69965

F70433

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ALIGNMENTS

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QY 241 AADPVEEIKVGFDILKSLRIRSRGINFIACPTCSRQEFDVIGTVNALEQRLEDIITPMDV 300	Qy 181 KASDVFLAVESYRLLAKQIDQPLHLGITEAGGARSGAVKSAIGLGLLLSEGIGDTLRVSL 240	Qy 121 VVDCARDKNIPIRIGVNAGSLEKDLQEKYGEPTPQALLESAMRHVDHLDRLNFDQFKYSV 180	Qy 61 VSVPTMDAAEAFKLIKQQVNVPLVADIHFDYRIALKVAEYGVDCLRINPGNIGNEERIRM 120	Qy 1 MHNQAPIORRKSTRIYVGNVPIGDGAPIAVQSMTNTRTTDVEATVNQIKALERVGADIVR 60	Query Match 100.0%; Score 1866; DB 1; Length 372; Best Local Similarity 100.0%; Pred. No. 1.3e-121; Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	A;Residues: 1-372 <blat> A;Residues: 1-372 <blat> A;Cross-references: GB:AE000338; GB:U00096; NID:g1788862; PIDN:AAC75568.1; PID:g17888 A;Experimental source: strain K-12, substrain MG1655 C;Genetics: A;Gene: gcpE C;Superfamily: gcpE protein</blat></blat>	A; Reference number: A64720; MUID:97426617; PMID:9278503 A; Accession: B65028 A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA		A; Molecule type: DNA A; Residues: 1-372 <bak> A; Cross-references: EMBL:x64451; NID:g41540; PID:g41542 A; Experimental source: strain K-12</bak>	R; Baker, J.; Franklin, D.B.; Parker, J. FEMS Microbiol. Lett. 94, 175-180, 1992 A; Title: Sequence and characterization of the gcpE gene of Escherichia coli. A; Reference number: S23057 A; Accession: S23058	S23058 S23058 S23058 Group Protein - Escherichia coli (strain K-12) Crispecies: Escherichia coli Crispecies: Escherichia coli Crispecies: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 01-Mar-2002 Criscession: S23058; B65028

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gasawara, N.; Yasunaga, T.; Kuha
DNA Res. 8, 11-22, 2001
A; Fittle: Complete genome sequence
A; Reference number: A99629; MUII
A; Accession: A91051
A; Status: preliminary
    hypothetical protein gcpE [impo
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_5
C;Accession: E88895
R;Perna, N.T.; Plunkett III, Go
iller, L.; Grotbeck, E.J.; David
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A; Molecule type: DNA
A; Residues: 1-372 <HAY>
A; Residues: 1-372 <HAY>
A; Cross-references: GB:BA0000076 PIDN:BAB36800.1; PID:g13362847; GSPDB:GN00154
A; Cross-references: strain 0057:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 2
A91051
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C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C;Accession: A91051
C;Accession:
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ihara, S.;
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                                                                        revision 16-Feb-2001
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          Burland, V.; Mau, B.; Glasner, N.W.; Lim, A.; Dimalanta, E.;
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Pred. No. 1.3e-121;
; Mismatches 0;
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Shiba, T.; Hat
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Hattori, N
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                                                                                                                 coli (strain
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Shinagawa,
             J.D.; Rose, Potamousis,
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Best Loca Matches

365;

Conservative

98

18,

score 1831; I Pred. No. 3.5e 4; Mismatches

DB :

Length

372;

Indels

0

Gaps

0;

Local Similarity

Query Match

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A;Molecule type: DNA
A;Residues: 1-372 <STO>
A;Cross-references: GB:AEO05174; NID:g12516909; PIDN:AAG57625.1;
A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 409, 529-533, 2001
A; Title: Genome sequence of
A; Reference number: A85480;
A; Accession: E85895
 A; Gene:
C; Superf
                                                                                                                                                                                                                                   GCPE protein (protein E) [imported] - Salmonella enterica subsp. enterica C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-200
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R; Parkhill, J.; Dougan, G.;
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                                                                                                                  A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; A; Title: Complete genome sequence of a multiple drug resistant A; Reference number: AB0502; MUID:21534947; PMID:11677608
                             A;Cross-references:
C;Genetics:
                                                         A; Molecule type: DNA
A; Residues: 1-372 < PAR>
                                                                                      A; Status: preliminary
                                                                                                   A; Reference number: AB0502;
A; Accession: AB0822
                                                                                                                                                               Nature 413,
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Best Local S
Matches 372
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                                                                                                                                                             h, T.; Connerton, P.; Croni
S.; Moule, S.; O'Gaora, P.
ature 413, 848-852, 2001
Superfamily:
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ilarity 100.0%;
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                                              GB:AL513382;
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                                                                                                                                                                                            James,
nin, A.;
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MUID:21074935; PMID:11206551
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                                               PIDN: CAD02726.1;
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Pred. No. 1.3e-121;
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Davis,
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                                                                                                                                                                                           Thomson, N.R.; Pickard, P.; Davies, R.M.; Dowd.
                                               PID:g16503738;
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                                                   GSPDB:GN00176
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A;Recession: Ag0350
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-375 <KUR>
A;Cross-references: GB:AL590842; PIDN:CAC92130.1; PID:g15980846; GSPDB:GN00 C;GenetLos:
A;Gene: aarC
C;Superfamily: gcpE protein
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C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001 C;Accession: AG0350 R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; P. R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; P. R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; P. R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; P. R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; P. R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; P. R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; P. R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; P. R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; P. R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; P. R;Parkhill, M.R.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; P. R;Parkhill, M.R.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; P. R;Parkhill, M.R.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; P. R;Parkhill, M.R.; W.R.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; P. R;Parkhill, M.R.; W.R.; W.R.
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    MHNQAPIQRRKSTRIYVGNVPIGDGAPIAVQSMINTRTTDVEATVNQIKALERVGADIVR
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Pred. No. 9.1e
19; Mismatches
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A; Map position:
C; Superfamily: 9
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A; Molecule type: DNA
A; Residues: 1-376 <HBI>
A; Cross-references: GB: AE004161;
A; Experimental source: serogroup
C; Genetics:
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C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision
C:Accession: F82283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Reference number: A82035; MUID:20406833; PMID:10952301 A;Accession: F82283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cpE protein VC0759 [imported] - Vibrio cholerae (strain species: Vibrio cholerae
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                                                 DEKNRIDIKHVEQ
               DEARRIDVQQVEK
                                                                                                             AADPVEEIKVGFDILKSLRIRSRGINFIACPSCSRQEFDVIGTVNALEQRLEDVLTPMDV
                                                                                                                            AADPVEEIKVGFDILKSLRIRSRGINFIACPTCSRQEFDVIGTVNALEQRLEDIITPMDV
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                                                                                                                                                                                                                                                                                        VVDCARDKGIPIRIGVNGGSLEKDLQLKYGEPTPEALVESAMRHVDILDRLNFDQFKVSV
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375
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                                                                                                                                                                                                                                                                                                                                                                                                            Score 1621.5; DB 2
Pred. No. 1.1e-104;
3; Mismatches 21;
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H.; Dragoi, I.; Sellers
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White,

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Clayton,

R.A.;

Kerlavage

(strain

Rd KW20)

10-Sep-1999 #text_change 28-Jul-2000

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A; Molecule type: DNA
A; Residues: 1-368 <TIGR>
A; Cross-references: GB:U32721; C; Genetics:
A; Gene: gcpE
C; Superfamily: gcpE protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Gocayne, J.D.; Scott, J.; Shipley, R.; Liu, L.I.; Glodek, A.; Kell, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Science 269, 496-512, 1995
A;Anthors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; SA;Ritle: Whole-genome random sequencing and assembly of Haemophilus A;Reference number: A64000; MUID: 95350630; PMID: 7542800
A;Accession: H64063
A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: Nua
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Nature 406, 959-964, 2000

A;Title: Complete genome sequence of Pseudomonas aeruginosa
A;Reference number: A82950; MUTD:20437337; PMID:10984043
A;Accession: F83171
A;Status: preliminary
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F83171
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C; Superfamily: gcpE protein
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                                                                                                                    A; Molecule type: DNA
A; Residues: 1-371 <STO>
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Matches
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Best Local :
                                                                                            Cross-references: GB:AE004798; Experimental source: strain PA
                                                                                  Genetics:
                       Best Local
                                   Query Match
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88.280
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73.88
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                                                                                                          GB:AE004091; NID:g9949963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1603.5; DB 1; Pred. No. 1.8e-103;
             Score 1372.5; DB 2;
Pred. No. 1.7e-87;
5; Mismatches 48;
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                                                                                                                                                                                                                                                                              Pseudomonas aeruginosa (strain
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                Indels
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                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   gcpE protein [imported] - Buchnera sp. (;Species: Buchnera sp. (;Species: Buchnera sp. (;Date: 02-Mar-2001) #sequence_revision (C;Accession: E84963 R;Shigenobu, S.; Watanabe, H.; Hattori,
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C; Superfamily: gcpE
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A; Residues: 1-368 <STO>
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A;Experimental source: strain APS
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Best Local S
Matches 242
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RISIPNLKAAESFKEIKKQTNVPLIADIHFDYRLALQAIKYGADCLRINPGNIGNKRRVS
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                 LAAHPTEEVKVGYDILKVLSLRARGINFIACPTCSRQEFDVINTVNQLEKNLEDISTPID
                              LAADPVEEIKVGFDILKSLRIRSRGINFIACPTCSRQEFDVIGTVNALEQRLEDIITPMD
                                                                            VKASDVFLAVESYRLLAKQIDQPLHLGITEAGGARSGAVKSAIGLGLLLLSEGIGDTLRVS
                                                                                                               EIISYAKDENIPIRIGVNAGSLEKDILKKYKIPTPDALVESAMRHIEYFDALNFNQFKVS
                                                                                                                           gcpE protein
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                                                                                                                                                                                                                                                           Score 1282; DB 2;
Pred. No. 3e-81;
5; Mismatches 57,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (strain APS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       M.; Sakaki,
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                                                                      GIALLLEGIGDTIRVS
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VVDAARERNIPIRIGVNAGSLEKDLQKKYGEPTPEALLESAMRHVDHLDKLDFQNFKVSV
                                                                                                                                VSVPTMDAAEAFKLIKQQVNVPLVADIHFDYRIALKVAEYGVDCLRINPGNIGNEERIRM
                                                                                                                                                                                                   MHNQAPIQRRKSTRIYVGNVPIGDGAPIAVQSMTNTRTTDVEATVNQIKALERVGADIVR
                                     SIIGCVVNGPGEALVSTLGVTGGNKKSGLYEDGVRKDRLDNNDMIDQLEARIRAKASQLD
                                                                                        KASDVFLAVESYRLLAKQIDQPLHLGITEAGGARSGAVKSAIGLGLLLLSEGIGDTLRVSL
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122
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                        360
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A;Title: Genome sequence of the endocellular bacterial symbiont of aphids A;Reference number: A84930; MUID:20445173; PMID:10993077 A;Accession: E84963 02-Mar-2001 #text_change 23-Mar-2001 Y.; Ishikawa, Length Buchnera

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A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: H87354
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C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C;Accession: H87354
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A; Residues: 1-383 <S'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Residues: 1-383 <STO>
Cross-references: GB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genetics:
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                                                                                                                                                                                                                                                        VNGPGEALMTDIGFTGGGAGAGMVYMAGKPDHKQSNEGMIDHIVDLVEKKAAEIQAAKAQ 373
                                                                                                                                                                                                                              VNGPGEALVSTLGVTGGNKKSGL-YEDGVRKDRLDNNDMIDQLEARIRAKASQLDEARRI 365
                                                                                                                                                                                                                                                                                                              LAVESYRLLAKQIDQPLHLGITEAGGARSGAVKSAIGLGLLLSEGIGDTLRVSLAADPVE 246
                                                                                                                                                                                                                                                                                                                                                                    DHGCSMRIGVNAGSLERELLEKYGEPCPDAMVESALNHARILQDHDFHEFKISVKASDPF
                                                                                                                                                                                                                                                                                                                                                                                      DKNIPIRIGVNAGSLEKDLQEKYGEPTPQALLESAMRHYDHLDRLNFDQFKVSVKASDVF 186
                                                                                                                                                                                                                                                                                                                                                                                                                                        DAAEAFKLIKQQVNVPLVADIHFDYRIALKVAEYGVDCLRINDGNIGNEERIRMVVDCAR 126
                                                                                                                                                                                                                                                                                                                                                                                                                         ESTAAFKTIAREAKVPLVADIHFHYKRGIEAAQAGAACLRINPGNIGSPDRVRDVIQAAR 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IQRRKSTRIYYGNVPIGDGAPIAYQSMTNTRTTDVEATVNQIKALERYGADIYRYSYPTM 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ITRRQSRKIRVGSVEVGGDAPISVQSMTNTLTSDAAATLEQIRQLEEAGADIVRVSCPDV
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57.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1042.5; DB 2;
Pred. No. 1.1e-64;
7; Mismatches 95;
                                                    14-Sep-2001 #text_change 30-Sep-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIDN:AAK22836.1; GSPDB:GN00148
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A; Experimental source: strain
                                                                                                                                                                                                                                                                               A;Title: Complete genome sequence of the alkaliphilic bacterium A;Reference number: A83650; MUID:20512582; PMID:11058132 A;Accession: A83825
                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-367 <STO>
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C; Superfamily:
                                                                                                                                                                         Superfamily:
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                                                                                                                      Matches
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                                                                                                                     Conservative
                                                                                                                                                                                                                GB:AP001511; GB:BA000004; NID:g10173727; 
be: strain C-125
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A; Molecule type: DNA
A; Residues: 1-349 <KUR>
A; Cross-references: GB:AE001437; PIDN:AAK79762.1;
A; Experimental source: Clostridium acetobutylicum
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Genome Sequence and Comparative Analysis of the A;Reference number: A96900; MUID:21359325; PMID:21359325 A;Accession: G97121 A;Status: preliminary
                                                                                                                                                                             DKNIPIRIGVNAGSLEKDLQEKYGEPTPQALLESAMRHYDHLDRLNFDQFKYSYKASDVF 186
                                                                                                                                                                                                                                                                                                                                      DAAEAFKLIKQQVNVPLVADIHFDYRIALKVAEYGVDCLRINPGNIGNEERIRMVVDCAR
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                                                                                                EIKVGFDILKSLRIRSRGINFIACPTCSRQEFDVIGTVNALEQRLEDIITPMDVSIIGCV
                                                                                                                                                                                                                                    EKNIPIRIGVNSGSLEKDILNKYKRVCSEALVESALNHVKILEDVNFNDIVISIKSSNVQ
                                                                                                                                                                                                                                                                                                                 DAASSLSEITKNVKLPVVADIHFDYRLALEAIKNGVSALRINPGNIGSKERVELVAKSAK
                                                                                                                                                                                                                                                                                                                                                                                         VNGPGEALVSTLGVTGGNKKSGLYEDGVRKDRLDNNDMIDQLEARI 352
                                                                         EVKVGREILKTFGYLKSGVEFISCPTCGRTSIDLIKIANEVEKRLEKTNKSIKVAVMGCV
                                                                                                                                                      MMIDSYRLISKEVNYPLHLGVTEAGTIWRGTIKSSIGIGTLLSEGIGDTIRVSLTGDPVE
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Pred. No. 5.6e-54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PID: g15024769;
ATCC824
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peptidoglycan acetylation gcpE [imported] C;Species: Bacillus halodurans Species: Bacillus halodurans
Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 Bacillus halodurans #text_change 15-Jun-2001 (strain C-125)

R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, Nucleic Acids Res. 28, 4317-4331, 2000 R.; Masui, N.; Fuji, Bacillus halodurans 12) . .

48.8%; 47.38; Score 882.5; | Pred. No. 1.2e 64; Mismatches); DB 2; L.2e-53; Length

PIDN:BAB05120

64;

Indels

7;

Gaps

RRKSTRIYVGNVPIGDGAPIAVQSMTNTRTTDVEATVNQIKALERVGADIVRVSVPTMDA AEAIPAIKKQISIPLVVDIHFDYKLALKAIEGGADKIRINPGNIGKRHKVEAVVKAAKEK AEAFKLIKQQVNVPLVADIHFDYRIALKVAEYGVDCLRINPGNIGNEERIRMVVDCARDK RTKTRPVKVGNLTIGGNNEVVVQSMTTTKTHDVEATVAEIKRLEEAGCQVVRVACPDMRA 99

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R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquel, Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Macok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boliok, Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUDD:21537279; PMID:11679669
A;Accession: AI1254
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-368 <GLA>
A;Cross-references: GB:NC_003200; PIDN:CAC99519.1; PID:9164.
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A; Gene: lmo1441
C; Superfamily: g
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C; Accession: AII254
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C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence revision 27-Nov-2001
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Matches 178
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Experimental source: strain EGD-e
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178; Conser
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             GPGEAREADIGIAGS
                                                           ANALSAIKKKIHIPLV
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49.28)
                                                                                                                       STOEKYGEPTPQALLESAMRHVDHLDRLNFDQFKVSVKASDVFLA 188
                                                                                                                                                                                                                                                VADIHFDYRIALKVAEYGVDCLRINPGNIGNEERIRMVVDCARDK 128
                                 WKKSGLYEDGVRKDRLDNNDMIDQLEARIRAKASQLDEARRIDVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chrieser, C.; Amend, A.; Baquero, Ind, E.; Durand, L.; Dussurget, O.;
                                                                                                                                                                                                                                 ADIHFDYRLALKAIDAGVDKIRINPGNIGRRDRVEKVVNAAKAK
          GEGLLFRHGKIIRKVPEAIMIDELKKEIDILAEEF-FVKKIDLE
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N.; Tierrez, A.; Vazquez-Boland, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ITEAGGARSGAVKSAIGLGLLLSEGIGDTLRVSLAADPVEEI 248
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                                                                                                                                                                                                                                                                                                                                             Score 868; DB 2;
Pred. No. 1.2e-52;
7; Mismatches 115;
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                                                                                                                                                                                                                                                                                                                                                                        Length 368;
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tian, K.D.;
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Voss, H.; W
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Fsihi, H.
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F70433
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C; Date: 05-Dec-1997 #sequence_revision
C; Accession: C69955
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C;Superfamily: gcpE protein
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A; Residues: 1-377 < KUN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary; nucleic acid sequence not shown; translation
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Pred. No. 4.9e-52;
6; Mismatches 115;
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C;Superfamily: gcpE protein
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A;Residues: 1-357 <AQF>
A;Cross-references: GB:AE000745; NID:g2983907; PIDN:AAC07467.1; PID:g2983917; GB:AE00065
A;Experimental source: strain VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 44.4%; Score 828; DB 2; L Best Local Similarity 47.6%; Pred. No. 6.9e-50; Matches 165; Conservative 73; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.;Reference number: A70300; MUID:98196666; PMID:9537320;Recession: F70433;Accession: F70433;Status: preliminary; nucleic acid sequence not shown; translation not shown
302 VNAIGEAREADIGLACGRGFAWLFKHGKPIKKVDESEMVDELLKEIQ 348
                                                        307 VNGPGEALVSTLGVTGGNKKSGLYEDGVRKDRLDNNDMIDQLEARIR 353
                                                                                                                                                                                       242 EVETAYEILKSLGLRRRGVEIVACPTCGRIEVDLPKVVKEVQEKLSGVKTPLKVAVMCCV 301
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                                                                                                                                                                                                                                                                              EIKVGFDILKSLRIRSRGINFIACPTCSRQEFDVIGTVNALEQRLEDIITPMDVSIIGCV 306
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Search completed: August 12, 2003, 09:56:50 Job time : 43 secs

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             Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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          GenCore version 5.1.6 (c) 1993 - 2003 Compus
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087516 vibrio para
08dez8 vibrio vuln
P72241 providencia
P58672 yersinia pe
09ktx1 vibrio chol
P44667 haemophilus
P57987 pasteurella
09hxj4 pseudomonas
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08d1y3 wiggleswort
09a8667 clostridium
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RX MEDLINE-21156331; PubMed-11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yoka RA Han C.-G., Ohtsubo E., NaKayama K., Murata T., Tanaka M., Tobe RA Iida T., Takami H., Honda T., Saskawa C., Ogasawara N., Yasun RA Kuhara S., Shiba T., Hattori M., Shinagawa H.; Xufara S., Shiba T., Hattori M., Shinagawa H.; Escherichia coli T. Olj57:H7 and genomic comparason with a laboratory strain K-12 T Olys 1:H and genomic comparason with a laboratory strain K-12 T DNA Res. 8:11-22(2001).
                                               Beck E., Jomas H.;

"GCPE is involved in the 2-C-methyl-D-erythritol 4-phosphate pathway of isoprenoid biosynthesig in Escherichia coli.";

J. Bacteriol. 183:2411-2306(2001).

-I. FUNCTION: Converts 265methyl-D-erythritol 2,4-cyclodiphosphate (ME-2,4CPP) into 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate.
-I. PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; sixth step.
-I. SIMILARITY: BELONGS TO THE ISPG FAMILY.

This SWISS-PROT entry is Copyright. It is produced through a collaborative of Bioinformatics and the EMBL outstation the European Bioinformatics Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on use by non-profit institute of Bioinformatics and the EMBL outstation the European Bioinformatics is not removed. Usage by and for commerciation and this statement is not removed. Usage by and for commerciation and this statement is not removed. Usage by and for commerciation and the statement is not removed. Usage by and for commerciation and the statement is not removed. Usage by and for commerciation and the statement is not removed. Usage by and for commerciation and the statement is not removed. Usage by and for commerciation and the statement is not removed. Usage by and for commerciation and the statement is not removed. Usage by and for commerciation and the statement is not removed. Usage by and for commerciation and the statement is not removed. Usage by and for commerciation and the statement is not removed. Usage by and for commerciation and the statement is not removed. Usage by and for commerciation and the statement is not removed. Usage by and for commerciation and the statement is not removed. Usage by and for commerciation and the statement is not removed. Usage by and for commerciation and the statement is not removed. Usage by and for commerciation and the statement is not removed. Usage by and for commerciation and the statement is not removed. Usage by and for commerciation and the statement is not removed. Usage 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-2109983; PubMed Mil63766; Campos N., Rodriguez-Concepcion M., "Identification of gcpE as a novel 4-phosphate pathway for 15oprenoid FEBS Lett. 488:170-173(2001).
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MEDLINE-22388234; PubMed-12471157;

Welch R.A., Burland V., Plunkett G. III, Redford P., Ro
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N
Mobley H.L.T., Donnenberg M.S.; Blattner F.R.;

"Extensive mosaic structure revealed by the complete ge
of uropathogenic Escherichia coli.";

proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
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MEDLINE=21099853; Pu
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biosynthesis in Escherichia coli.";
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ID ISPG_S
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DT 28-FEB
CO SALMON
OC BACTEC
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RN [1]
RP SEQUEN
RC STRAIN
RX MEDLIN
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HAMAP; ME_00159;
InterPro; IPR004588; Ispg.
InterPro; IPR004581; 1.
Pfam; PF04551; GcpE; 1.
TIGREAMS; TIGR00612; ispg_gcpE; 1.
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                   SEQUENCE FROM N.A.
STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=2154948; PubMed=11677609;
MCClelland M., Sanderson K.E., Spleth J.
Courtney L., Porwollik S., All J., Dante
Leonard S., Nguyen C., Scott K., Holmes
Ryan E., Sun H., Florea L., Miller W., S
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Enterobacteriaceae; Salmonella.
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L; AE005481; AAG57625.1; -.
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StyGene; SG7????; 1spG.
HAMAP; MF_00159; -; 1.
InterPro; IPR006705; GcpE.
InterPro; IPR004588; IspG.
Pfam; PF04551; GcpE; 1.
TIGREAMS; TIGR00612; 1spG_gcpE; 1.
Isoprene blosynthesis; Complete pr
SEQUENCE 372 AA; 40625 MW; 048
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                                                                                                                           ISPG_SALTI STANDARD; PRT; 372 AA. P-8670; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 15-FEP-2003 (Rel. 42, Last annotation update) 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate ISPG OR GCPE OR STY2768 OR T0333. Salmonella typhl.
                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae; Salmonella.
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Nature 413:852-856(2001).

Nature 413:852-856(2001).

'I FUNCTION: Converts 2C-methyl-D-erythritol 2,4-cyclodiphosphate (ME-2,4cPP) into 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate (By similarity).

(By similarity).

Nonmevalonate terpenoid biosynthesis pathway; sixth steries (BY SIMILARITY: BELONGS TO THE ISPG FAMILY.
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InterPro; IPR004588; IspG.
Pfam; PF04551; GcpE; 1.
TIGRFAMS; TIGR00612; ispG_gcpE; 1.
Isoprene biosynthesis; Complete pr
SEQUENCE 372 AA; 40626 MW; 3E;
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-i-FUNCTION: Converts 2C-methyl-D-erythritol 2,4-cyclodiphosphate (ME-2,4cPP) into 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate (By similarity).

-i- PACHWAY: Nonmevalonate terpenoid biosynthesis pathway; sixth steries (By SIMILARITY: BELONGS TO THE ISPG FAMILY.
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EMBL; AE016835; AA068056.1;
HAMAP; MF_00159; -; 1.
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STRAIN-TY2 / ATCC 700931;
MEDLINE-25931867; PubMed=12644504;
Deng W., Liou S.-R., Flunkett G. III, Mayhew G.F.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner
"Comparative genomics of Salmonella enterica serova
and CT18.";
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STRAIN-RIMD 221033 / Serogype 03:K6;
MARINE 2508454; PubMed 10:620739;
MARINE K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Ta Marine K., Najima M., Nakano M., Yamashita A., Kubota Y., Yiliana Y., Najima M., Nakano M., Yamashita A., Kubota Y., Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
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            RIRSRGINFIACPTCSRQEFDVIGTVNALEQRLEDIITPMDV
                                                                                                                                                                                                                                                                                                                                                                                                                       Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1645.5;
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Choy H.E.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGREAMS; TIGRO0612; ispG_gcpE; Isporene biosynthesis; Complete SEQUENCE 372 AA; 4057
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15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
1-hydroxy-2_methyl-2-(E)-butenyl 4-diphosphate
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(By similarity).

PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; sixth step.

SIMILARITY: BELONGS TO THE ISPG FAMILY.
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320; Conserv
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                    AADPVEEIKVGFDILKSLRIRSRGINFIACPTCSRQEFDVIGTVNALEQRLEDIITPMDV
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  AANPVEEIKVGFDILKSLRIRSRGINFIACPSCSRQEFDVISTVNALEERLEDIITPMDV
                                                                                                                                                      VVDCARDKNIPIRIGVNGGSLEKDLQMKYGEPTPEALVESAMRHVDILDRLNFDQFKVSV
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86.7%;
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                                                                                                                                                                                                                                                                                                                                                                                             29;
                                                                                                                                                                                                                                                                                                                                                                                                         Score 1631.5;
Pred. No. 2.66
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6C73C2B8819B0285 CRC64;
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"aarC, an essential gene involved in density-dependent regulation of
the 2'-N-acetyltransferase in providencia stuartii.";

J. Bacteriol. 179:2267-227311997).

-I- FUNCTION: Converts 2C-methyl-D-erythritol 2,4-cyclodiphosphate
(ME-2,4cPP) into 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate
(By similarity). Involved in density-dependent regulation of 2'-N-
acetyltransferase.

-I- PANHWAY: Nonmevalonate terpenoid biosynthesis pathway; sixth step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U67933; AAB51469.1;
HAMAP; MF_00159; -; 1.
InterPro; IPR004588; IspG.
Pfam; PF04551; GCPE; 1.
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16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate
ISPG OR AARC.
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            KASDVFLAVESYRLLAKQIDQPLHLGITEAGGARSGAVKSAIGLGLLLSBGIGDTLRVSL
                                                                                MHNQAPIQRRKSTRIYVGNVPIGDGAPIAVQSMINTRTTDVEATVNQIKALERVGADIVR
                                                                                                                                                                                  VSVPTMDAAEAFKLIKQRVNVPLVADIHFDYRIAMKVAEYGVDCLRINPGNIGSEERIRQ
                                                                                                                                                                                                            VSVPTMDAAEAFKLIKQQVNVPLVADIHFDYRIALKVAEYGVDCLRINPGNIGNEERIRM
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Providencia.
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STRAIN=CO-92 / Biovar Orientalis;

RX MEDLINE-21470413; PubMed-11586360;

RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,

RA Prentice M.B., Sebalhia M., James K.D., Churcher C., Mungall K.L.,

RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,

RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,

RA Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,

RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,

RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;

"Genome sequence of Yersinia pestis, the causative agent of plague.";

RL Nature 413:533-527(2001).
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                                                                                                                 the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                     EMBL; AJ414154; CAC92130.1;
EMBL; AE013738; AAM84926.1;
PIR; AG0350; AG0350.
HAMAP; MF_00159; -; 1.
                                                                                                                                                                                                                                                                          "Genome sequence of Yersinia pestis KIM.";

J. Bacteriol. 184:4601-4611(2002).

-I- FUNCTION: Converts 2C-methyl-D-erythritol 2,4-cyclodiphosphate

(ME-2,4cPP) into 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-KIM5 / Biovar Mediaevalis;
MEDLINE-22137863; PubMed-12142430;
Deng W., Burland V., Plunkett G. III, Boutin A.,
Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz
Fetherston J.D., Lindler L.E., Brubaker R.R., Pla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yersinia pestis.
Bacteria; Proteobacteria;
Enterobacteriaceae; Yersi
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
1-hydroxy--methyl-2-(E)-butenyl 4-diphosphate
ISPG OR GCPE OR YPO2879 OR Y1353.
                                                                                                                                                                                                                                                                                                                                              Straley S.C., McDonough K.A.,
Perry R.D.;
                                                                                                                                                                                                                                (ME-2,4cPP) into 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate (By similarity).
PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; sixth step.
SIMILARITY: BELONGS TO THE ISPG FAMILY.
                                                                                                                                                                                                                 SWISS-PROT entry is
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tute of Bioinformatics
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                                                                                                                                                                                                            is produced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  causative agent of plague.";
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Matson J.S., E
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InterPro; IPR006705; (InterPro; IPR004588; Pfam; PF04551; GcpE; TIGRFAMS; TIGR00612;

: 1. GCPE. : IspG.

ispG_gcpE;

SS

Isoprene SEQUENCE

Matches Query Match Best Local

323;

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-i- PATHMAY: Nonmevalonate terpenoid biosynthesis pathway:
-i- SIMILARITY: BELONGS TO THE ISPG FAMILY.

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           restrictions
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SEQUENCE FROM N.A.

STRAIN-E1 TOR N16961 / Segetype 01;

STRAIN-E1 TOR N16961 / Segetype 01;

MEDLINE-20406833; PubMed-10952301;

Heidelberg J.F., Eisen J.D., Nelson W.C., Clayton R.A., Gwindols R.J., Haft D.H., Hickey E.K., Petterson J.D., Umayam Bodson R.J., Heith L.H., Hickey E.K., Petterson J.D., Umayam Gill S.R., Nelson K.B., Read T.D., Tettelin H., Richardson Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., McDonald L., Utterback T.D. Fleischmann R.D., Nierman W.C., Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Verser C.M.;
                                                                                            Nature 406:477-483(2000).

Nature 406:477-483(2000).

-I- FUNCTION: Converts 205methyl-D-erythritol 2,4-cyclodiphosphate

(ME-2,4cPP) into 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate

(By similarity).

(By similarity).
                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Vibrionaceae; Vibrio. NCBI_TaxID=666;
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
1-hydroxy-2-methyl-2-(E)-bitenyl 4-diphosphate synthase.
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375 AA; 40797
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86.8%
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19; Mismatches 29;
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860971872B1C0536 CRC64;
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                                 gh a collaboration EMBL outstation -
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D.,
                                                                                         sixth step.
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ISPG_HAEIN
ISPG_HAEIN
1667;
SEQUENCE FROM N.A.

RC STRAIN=8d / KW20 / ATCC 51907;

RC STRAIN=8d / KW20 / ATCC 51907;

RX MEDILINE-95350630; PubMede-7542800;

RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

RA Weidman J.F., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M.
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Matches
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InterPro; IPR004588;
Pfam; PF04551; GcpE;
TIGRFAMS; TIGR00612;
                                                                                                                                                                                                                                                                                         P44667;
01-NOV-1995
01-NOV-1995
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pfam; pF04551; GcpE; 1.
pfam; pF04551; GcpE; 1:
programs; TIGR00612; ispG_gcpE;
Isoprene biosynthesis; Complete
SEQUENCE 376 AA; 40862 MW; 3
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                                                                                                                                                                                                      01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate
1spG OR GCPE OR HI0368.
1spG OR GCPE OR HI0368.
Bacteria; Proteobacteria; Gammaproteobacteria;
Pasteurellaceae; Haemophilus.
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Local 318;
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AAF93924.1;

proteome.
34E4144CBB7ADAAA

CRC64;

Conservative 85.3%; 33; Score 1621.5; Pred. Mismatches No. 1 .5; DB 1; 1.3e~104; hes 21; Indels Length 376; ۲, Gaps

QY 밁 δÃ 맑 δÃ

> 61 61

62

180 122 120

182 240

AADPVEEIKVGFDILKSLRIRSRGINFIACPTCSRQEFDVIGTVNALEQRLEDIITPMDV 300 242

SIIGCYVNGPGEALVSTLGVTGGNKKSGLYEDGVR-KDRLDNNDMIDQLEARIRAKASQL 302

362

375

STANDARD; 368 A

Pasteurellales;

synthase

,4-cyclodiphosphate

4-diphosphate

Pm70.

Kapur V.;

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RESULT 10
ISPG_PARMU
ID ISPG_P
P57987
P7 16-OCT
DT 16-OCT
DT 16-PEB
DE 1-hydr
GN ISPG O
OS Pasteu
OC Pasteu
OX NCBI_T
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Matches 320
                                                                                       ISPG_PASMU STANDARD; PRT; 367
P57987;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence upda
28-FEB-2003 (Rel. 41, Last annotation update)
1-hydroxy-2-methyl-2-(E)-butenyl 4-dipha
ISPG OR GCPE OR PM2010.
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PIR; H64063; H64063.
TIGR; H10368; -.
HAMAP; ME_00159; -; 1
                                                       Pasteurella multocida.
Bacteria; Proteobacteria;
                Pasteurellaceae;
NCBI_TaxID=747;
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InterPro; IPR004588; IspG.
Pfam; PF04551; Gcpg; 1.
TIGREAMS; TIGR00612; 1spG_gcpE; 1.
Isoprene biosynthesis; Complete pr
SEQUENCE 368 AA; 40116 MW; DC9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for continuities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 269:496-512(1995)
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By Similarity),
PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; sixth step.
SIMILARITY: BELONGS TO THE ISPG FAMILY.
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4cPP) into 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate
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                                                  Gammaproteobacteria;
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Pred. No. 2.1e-103;
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DC99EA15A50ED01B
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                                                                                                                            TSPG_PSEAE STANDARD; PRT; 371 AA. 09HXJ4; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate ISPG OR PA3803.
  SEQUENCE
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SEQUENCE FROM N.A.
STRAIN-PM70;
MEDLINE-21145866; PubMed-11248100;
MEDLINE-2145866; PubMed-11248866; Pub
                                                                              Pseudomonas aeruginosa.
Bacteria; Proteobacteria;
                                       NCBI_TaxID=287;
                                                           Pseudomonadaceae;
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Isoprene biosynthesis; Complete proteome.
SEQUENCE 367 AA; 39969 MW; 1918C5702642AEE8 CRC64;
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HAMAP; MF_00159; -; 1.
InterPro; IPR00458; IspG.
Pfam; PF04551; GCPE; 1.
TIGREPAMS; TIGR00612; 1spG_gc
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-!- FUNCTION: Converts 2C-methyl-D-exythritol 2,4-cycl (ME-2,4cpp) into 1-hydroxy-2-methyl-2-(E)-butenyl
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                                                                           Gammaproteobacteria;
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Pred. No. 4e-103;
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MEDLING-20437337; Pubmed-10984043;

MEDLING-20437337; Pubmed-10984043;

Hickey M.J., Brinkman F.S. M., Hufnagle W.O., Kowalik D.J., Lagrou M., Barber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Edyger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.";

Nature 406:959-964(2000).

Nature 406:959-964(2000).

Nature 406:959-964(2000).
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PIR; F83171; F83171.
HAMAP; MF_00159; -; 1.
InterPro; IPR004588; IspG,
Pfam; PF04551; GcpE; 1.
TIGRPAMS; TIGR00612; ispG_GcpE; 1.
Isoprene biosynthesis; Complete proteome.
Isoprene 371 AA; 40056 MW; F33FC1FCEF017117 CRC64;
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ISPG_BUCAP
Q8K9P4;
28-FEB-2003
28-FEB-2003
                                                   BUCAP
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SIMILARITY: BELONGS TO THE ISPG FAMILY.
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267; Conserv
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                                        STANDARD;
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73.880
 Created)
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    sequence update)
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Pred. No. 1.7e
                                        PRT;
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Lagrou M.,
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1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase.
1SPG OR GCPE OR BUGG276.
Buchnera aphidicola (subsp. Schizaphis graminum).
Bacteria; Proteobacteria; Gammaproteobacteria; EnterobacEnterobacteriaceae; Buchnera.
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Tamas I., Klasson L., Canbaeck B., Naeslund A.K., Eriksson A.-S.,
Wernegreen J.J., Sandstroem J.P., Moran N.A., Andersson S.G.E.;
"50 million years of genomic stasis in endosymbiotic bacteria.";
"50 million years of genomic stasis in endosymbiotic bacteria.";
Science 296:2376-2379(2002)
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InterPro; IPR006705; GCPE.
InterPro; IPR006788; ISPG.
Pfam; PF04551; GCPE; 1.
TIGRFANS; TIGR00612; ispG_gCPE; 1.
TIGRFANS; TIGR00612; Complete proteome.
Isoprene biosynthesis; Complete proteome.
SEQUENCE 367 AA; 40440 MW; 4CF6A0FAF017661C CRC64;
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PATHWAY: Nonmevalonate terp
SIMILARITY: BELONGS TO THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VSVPTMDAAEAFKLIKQQVNVPLVADIHFDYRIALKVAEYGVDCLRINPGNIGNEERIRM
                                                                                                                                                                                                                                                                                        KTSDVFSAIEANEILAKKTVQPIHIGITESGALRNGIVKSSIGITSLLLSGIGDTLRISL
                                                                                                                                                                                                                                                                                                                                                                                                                         MNKYKNIKRRKSNRIYVGNVPIGDGAPISVQSMINTQTINIEETIKQIIKLKKVGVDIVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MHNQAPIQRRKSTRIYYGNVPIGDGAPIAVQSMTNTRTTDVEATVNQIKALERVGADIVR
                                                                                                                                                                                                             SIIGCVVNGPGEALVSTLGVTGGNKKSGLYEDGVR-KDRLDNNDMIDQLEARIRAKASQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIIGCIVNGIGEAKVSTLGIVGGSKTSALYKDGIRQKNKLKNQEIIKELEIKIRKKAKSL
                                                                                  DKLKKI
                                                                                                                                      DEARRI 365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         terpenoid biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1285.5; DB
Pred. No. 1.6e-81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISPG FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pathway; sixth step.
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ISPG_BUCAI

ISPG_BUCAI

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Best Local
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HANMAP; ME_00159; -; 1.
InterPro; IPR004588; IspG.
Pfam; PF04551; GcpE; 1.
TIGRPAMS; TIGR00612; ispG_gcpE; 1.
ISOPTENE blosynthesis; Complete prot
SEQUENCE 368 AA; 40869 MW; 8BC3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=TOKYO 1998;
MEDLINE=20445173; PubMed=10993077;
Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa
Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AP001118; BAB12997.1; HSSP; P49058; 1EEP. HAMAP; MF_00159; -; 1. InterPro; IPR004588; IspG. Pfam; PF04551; GcpE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. APS.";
Nature 407:81-86(2000).
-I- FUNCTION: Converts 2C-methyl-D-erythritol 2,4-cyclodiphosphate (ME-2,4cPP) into 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate (By similarity).
-I- PANHWAY: Nonmevalonate terpenoid biosynthesis pathway; sixth step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon psymbiotic bacterium).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-CCT-2001 (Rel. 40, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate
ISPG OR GCPE OR BU287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enterobacteriaceae;
 361
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                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                            LNNSKK 366
                            LDEARR
                                                VSIIGCVVNGIGESKIATLGLAGSHKKSAFYEDGVRQKEKIKNEEIIEKMEIKIRKKIDK
                                                                  VSIIGCVVNGPGEALVSTLGVTGGNKKSGLYEDGVR-KDRLDNNDMIDQLEARIRAKASQ
                                                                                                                                                                                                                    EIISYAKDENIPIRIGVNAGSLEKDILKKYKIPTPDALVESAMRHIEYFDALNFNQFKVS
                                                                                                                                                                                                                                     MVVDCARDKNIPIRIGVNAGSLEKDLQEKYGEPTDQALLESAMRHVDHLDRLNEDQFKVS
                                                                                                                                                                                                                                                                            RISIPNLKAAESFKEIKKQTNVPLIADIHFDYRLALQAIKYGADCLRINPGNIGNKRRVS
                                                                                                                                                                                                                                                                                           RVSVPTMDAAEAFKLIKQQVNVPLVADIHFDYRIALKVAEYGVDCLRINPGNIGNEERIR 119
                                                                                                                                                                                                                                                                                                                                  MHNQAP-IQRRKSTRIYYGNVPIGDGAPIAVQSMTNTRTTDVEATVNQIKALERYGADIV
                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
                                                                                                                                                                                                                                                                                                                                                                                          68.7%; Score 1282; DB 1; L 66.1%; Pred. No. 2.9e-81; ** Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Buchnera
                                                                                                                                                                                                                                                                                                                                                                                                                                                   e proteome.
8BC32F495954C1DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        synthase
                                                                                                                                                                                                                                                                                                                                                                                                                        Length 368;
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aphids
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RESULT 14
ISPG_WIGBR
ID ISPG_W
AC 08D1Y3
DT 15-SEP
DT 15-SEP
DT 15-SEP
DT 15-SEP
DT 15-SEP
CC Entero
OX Wiggle
OC ENCELT
RN [1]
RP SEQUEN
RX MEDLIN
RA Aksoy
RT flies,
RL Nat. G
CC -!-FU
CC -!-FU
CC -!-FU
CC -!-SC
CC -!-PA
CC -!-
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Best Local S
Matches 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF04551; GcpE; 1.
TIGRPAMS; TIGRO0612; ispG_gcpE; 1.
Isoprene biosynthesis; Complete proteome.
SEQUENCE 366 AA; 40407 MW; 159E0169EBFC8DED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nat. Genet. 32:402-407(2002).
-i- FUNCTION: Converts 2C-methyl-D-erythritol 2,4-cyclodiphosphate
(ME-2,4cPP) into 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AB063522; BAC24719.1;
HAMAP; MF_00159; -; 1.
InterPro; IPR006705; GcpE.
InterPro; IPR004588; IspG.
Pf4m; PF04551; GcpE; 1.
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15-SEP-2003
15-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    flies, Wigglesworthia glossi
Nat. Genet. 32:402-407(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Akman L., Yamashita A., Watanabe Aksoy S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=22297718; PubMed=12219091;
MEDLINE=22297718; PubMed=12219091;
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Wigglesworthia glossinidia brevipalpis.
Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Wigglesworthia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
1-hydroxy-2-methyl-2-(E) butenyl 4-diphosphate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (By similarity).

PATHWAY: Nonmevalonate terpenoid biosyn
SIMILARITY: BELONGS TO THE ISPG FAMILY.
                                                       307
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          307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 65.9
34; Conservative
                                          VNGPGEALVSTLGVTGGNKKSGLYEDGVR-KDRLDNNDMIDQLEARIRAKASQLD
                                                                                         TCVQSYKLLASKIDQPLHLGITESGSMLHGSIKSSIGIGLLLSEGIGDTLRVSLAADPIE
                                                                                                                                                                                                                                                                                                                      sequence of the endocellular vigglesworthia glossinidia.";
                                                                                                                                                                                                                     LAVESYRLLAKQIDQPLHLGITEAGGARSGAVKSAIGLGLLLLSEGIGDTLRVSLAADPVE
|:||:||:|||:|||||||||||:|
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                                                                                                                                                                                                                                                                                                                                                                                                                           DAAEAFKLIKQQVNVPLVADIHFDYRIALKVAEYGVDCLRINPGNIGNEERIRMVVDCAR
VNGLGEANRADIGISGSRNKSILFENGLRNNNKINNEEIIDKLEKYIRKKVKILN
                                                                                                                                                                                                                                                                                                                                                                                              EAAESFKIIKRNVSIPIVADIHFDYRIALKAAEYGADCLRINPGNIGKLNRIISVVSTAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1226.5; DB
Pred. No. 1.9e-77
2; Mismatches 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        biosynthesis pathway; sixth step
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 366;
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RESULT 15
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A Nierman W.C., Feldblyum T.W., Laub M.T., Paulsen I.T., Nelson K.E.,

A Risen J., Heidelberg J.F. Alley M.R.K., Ohta N., Maddock J.R.,

A Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

DeBoy R.T., Dodson R.J., Dürkin A.S., Gyinn M.L., Haft D.H.,

A Rolonay J.F., Smit J. Crayen M.B., Khouri H., Shetty J., Berry K.,

A Kolonay J.F., Smit J. Crayen M.B., Vamathevan J., Ermolaeva M., White O.,

Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.,

Tomplete genome sequence of Caulobacter crescentus.",

**Complete genome sequence of Caulobacter crescentus.",

**Proc. Natl. Acad. Sci. U.S.A. 98:4136-414(2001)

C. (ME-2,4cpp) into 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate

(By similarity)

C. (By similarity): Thydroxy-2-methyl-2-(E)-butenyl 4-diphosphate

C. (SIMILARITY: BELONGS TO THE ISPG FAMILY.
                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 208; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Detween the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics and the EMBL outstation the European Bioinformatics and the EMBL outstation on the suse by non-profit institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license elsb-sib.ch).

WHEL: AE005761; AAK22836.18 ...

TER: H87354; H87354.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    w.u-u.id; Proteobacteria; ∰phaproteobacteria; Caulobacterales;
Caulobacteraceae; Caulobac<u>te</u>er.
NCBI Ta∀TD-1550^^
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                                                                                                                                                                                                                                                                                                                                                                        TIGREAMS; TIGRO0612; ispG_gcpE; 1.
Isoprene biosynthesis; Complete proteome.
SEQUENCE 383 AA; 40788 MW; 8468EB400E
                                                                                                                                                                                                                                                                                                                                                                                                                         TIGR; CC0851; -, 1
HAMAP; MF_00159; -; 1
InterPro; IPR004588;
Pfam; PF04551; GCPE;
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ISPG OR CC0851.
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28-FEB-2003 (Rel. 41, Last Sequence update)
28-FEB-2003 (Rel. 41, Last Sequence update)
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                                     MTVAAYYQLAEAIDCF
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.ERELLEKYGEPCPDAMVESALNHARILQDHDFHEFKISVKASDPF 193
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Pred. No. 9.2e.
57; Mismatches
     GINFIACPTCSRQEFDVIGTVNALEQRLEDIITPMDVSIIGCV
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          306
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Search completed: August 12, 2003, 09:54:29
Job time: 25 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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-Q-/Ggn2_1/WSPTC_Spool/US09921992/runat_12082003_094912_17379/app_query.fasta_1.519
-QB-EST -QFMT=fastap -SUFFIX-rst -MIRMATCH-0.1 -LOOPCL-0 -LOOPEXT-0
-UNITS-bits -START=1 -END--1 -MATRIX-blosum62 -TRANS-human40.cdi -LIST-45
-DCCALIGN=200 -THR_SCORE-pct -THR_MAX-100 -THR_MIN-0 -ALIGN-15 -MODE-LOCAL
-QUTEMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-200000000
-USER-US09921992_@CGN_1_1_2810_crunat_12082003_094912_17379 -NCPU-6 -ICPU-3
-NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -DSPBLOCK-100 -LONGLOG
-DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOP-6
-FGAPEXT-7 -YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7
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Maximum Match 100%
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-MODEL=frame+_p2n.model -DEV=x1h
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Maximum DB
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1866
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gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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A523388 244Pb602 A523388 224Pb602 A1482869 EST442112 A1482869 EST4261192 BQ075044 QHI18D05 AV626844 AV626844 BE924238 EST428007 BU048059 PP_LEA003 BG99681 EST516532 B1933447 EST553336 BG525868 53-47-1-2 BQ862800 QGC22B19 CB621771 UCRCS01_0 CB621771 UCRCS01_0 CB621771 UCRCS01_0 CB791771 UCRCS01_0 CB791770 046F07AF BM059608 KS01002E0 BQ591926 E012583-0 BG124857 EST47053 AW738400 EST339867 CB662235 OSJNEG06B AV644003 AV644003 AV644808 AV642898 AV626792 AV626792	CB628479 OSIIEb04B CA022320 H243M1r BJ481080 BJ481080 BG591263 EST499105 Aul86794 Porphyra AW042702 ST23E04 P BJ551332 BJ55133 AV917069 AV917069 BJ465443 BJ465443 AV934187 AV934187 BQ080994 Sm112909, AUG552386 AUG52386	E120088 EST540823 B1235010 PH_05_x S B4235010 PH_05_x S A2570993 281PvD07	msh2_461 OSJNEe02 OSJIEa03 Zea mays	script

ALIGNMENTS

REFERENCE	SOURCE ORGANISM	KEYWORDS	VERSION	ACCESSION	•	DEFINITION	Locus	BZ575759	RESULT 1
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas. 1 (bases 1 to 1323)	Pseudomonas aeruginosa Pseudomonas aeruginosa	GSS.	BZ575759.1 GI:27210820	BZ575759 ·	genomic survey sequence.	uginosa genomic clo	BZ575759 1323 bp DNA linear GSS 17-DEC-2002		

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University of Washington
Box 352145, Seattle, WA 9
Tel: 2062216954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Whole-Genome-Sequence variation among multiple isolates of Psedomonas aeruginosa library
J. Bacteriol., (2002) In press
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Burns, J.L., K
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Chris K. Raymond
                                                                                                                                                                                                                                 GlyValAsnAlaGlySerLeuGluLysAspLeuGlnGluLysTyrGlyGluProThrPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                GlnPheLysValSerValLysAlaSerAspValPheLeuAlaValGluSerTyrArgLeu
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                                                                                                                                             ThrLeuArgValSerLeuAlaAlaAspProValGluGluIleLysValGlyPheAspIle
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                                                                                            LeuLysSerLeuArgIleArgSerArgGlyIleAsnPheIleAlaCysProThrCysSer
                                CGGCAGAACTTCGACGTGGTGAAGACCATGAACGAGCTGGAAGGGCGCCTGGAGGACCTG
                                                ArgGlnGluPheAspValIleGlyThrValAsnAlaLeuGluGlnArgLeuGluAspIle
                                                                                  CTCAAGTCCCTGCACCTGCGCTCCCGTGGCATCAACTTCATCGCCTGCCCGAGCTGTTCG
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/strain="MSH"
/db_xref="taxon:287"
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394
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/note="Environmental isolate.
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RESULT 2
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AUTHORS
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US-09-921-992-78 (1-372) x CB669733
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Em
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 828)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield
Kudrna,D., Dean,R., Soderlund,C., Wing,R. ar
Large-scale identification of ESTs involved
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BACKWARD: gga aac agc tat gac cat g
Plate: 02 row: H column: 05
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                                                                                                                                                                                                                                       /db_xref="taxon:39947"
/clone="OSJNEe02H05"
/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
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/note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
xhoI; 24 hrs after innoculation with Rice Blast (70-15)"
xhoI; 24 hrs after innoculation with Rice Blast (70-15)"
xhoI; 217 g 224 t 1 others
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/mol_type="mRNA"
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           Arizona Genomics Inst.
University of Arizona
Biological Sciences We
85721-0088, USA
                                                                                                                                                                          Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                           CB619369 853 bp mRNA OSIIEA03003.f OSIIEA Oryza sativa (indica clone OSIIEa03003 5', mRNA sequence.
                                                                                                        Jantasuriyarat, C., Lu, G., Gowda, M., Hatfield, J., Zhou, B., Mazur, Kudrna, D., Dean, R., Soderlund, C., Wing, R. and Wang, G. Large-scale identification of ESTs involved in the interaction
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                                                                 Contact: Rod Wing
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FORWARD: gta aaa cga cgg
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                    LeuLeuSerGluGlyIleGlyAspThrLeuArgValSerLeuAlaAlaAspProValGlu
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     CTTCTGATGGATGGCTTGGGCGATACAATCCGTGTCTCCCTCACGGAACCACCTGAAGAA
                                                           GTTACAGAAGCTGGAGAGGGTGAAGATGGGAGGATGAAGTCTGCCATTGGCATTGGAACA
                                                                              IleThrGluAlaGlyGlyAlaArgSerGlyAlaValLysSerAlaIleGlyLeuGlyLeu :::||||||||||||||
                                                                                                                  TATCGCTTGCTTGTAGCAGAAATGTATAACCTAGGGTGGGATTATCCTTTGCACTTGGGA
                                                                                                                                             TyrArgLeuLeuAlaLysGlnIle-----
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                                                                                                                                                                         GACTTCCATAACTTTGTGTTTTCAATGAAAGCAAGTAACCCTGTTATCATGGTCCAAGCA
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168 c
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/note="Vector: pBluescript
/note="Vector pBluescript
XhoI; Lesion Mimic SPL 11"
168 c 223 g 240 t
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/dev_stage="3 week"
/lab_host="DH10B"
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/mol_type="mRNA"
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/clone="OSIIEa03003"
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Zea mays PCC
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If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize CDNA sequences is either Virginia Walbot, Stanford or Pat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hainey, C.F., Dolan, M., Miao, G.H., Arthur, L.W., Hanafey, M., Morgante
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 1442)
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Mapping Project;

374 g 399 t 6 others
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                                                                                                                                                                                                                                                                                               GSS.
                University of Washington
Box 352145, Seattle, WA
Tel: 2062216954
Fax: 2066857244
                                                                                                                                                                   Spencer, D.H., Raymond, C.K., Smith, Burns, J.L., Kaul, R. and Olsen, M.V.
                                                                                                                                                                                                                                                                                                               BZ569685.1
                                                                                      Genome Center
                                                                                                      Contact: Chris K.
                                                                                                                        Psedomonas aeruginosa library
J. Bacteriol., (2002) In pre
                                                                                                                                                          Whole-Genome-Sequence variation
                                                                                                                                                                                                                                                         Pseudomonas aeruginosa
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craymond@u.washington.edu
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Smith, E.E., among

Sims, E.E.,

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                                                                                                                                                                                                                                                                    sPro-ThrCysSer-ArgGlnGlu-PheAspValIleGlyThrVal-AsnAlaLeuGluG
                                                                                                                                                                                                                                                    TTCGGACATCCTTAAGTTCCCTGAACCTTGCGCTCCCGTGGCATAAAACTCCATTGCTTG
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                                               luAlaArgIleArgAlaLysAlaSerGlnLeuAspGluAla
                                                                                    TGTATATCGACGGCAAGCCGTCGCAGAAACTGACCAACGACAACCTGGTGGACGAGCTGG
                                                                                                           euTyrGluAspGlyValArgLysAspArgLeuAspAsnAsnAspMetIleAspGlnLeuG
                                                                                                                                        GTCCGTGCGAAGCCAAGGAGGCCCATGTCGGCCTCACCGGCTGCACTCCGAACCTG----G
                                                                                                                                                                  lyProGlyGluAlaLeuValSerThrLeuGlyValThrGlyGlyAsnLysLysSerGlyL
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/mol_type="genomic DNA"
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/clone="pacs2-164_970"
/clone_11b="pacs2-164"
/note="clinical isolate 2-164 Whole
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Conservative:
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VERSION
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                                                                                 US-09-921-992-78 (1-372) x BI920888 (1-579)
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
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100 TyrGlyValAspCysLeuArgIleAsnProGlyAsnIleGlyAsn--
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EST.
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                                           AsnValProLeuValAlaAspIleHisPheAspTyrArgIleAlaLeuLysValAlaGlu
                           AACATCCCTCTGGTGGCTGACATTCATTTTGCTCCTTCTGTTGCACTTCGAGTGGCGGAG
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579 bp mRNA 11
EST540823 potato microtubers, in vitro-grown
clone cSTE26D20 5' end, mRNA sequence.
BI220888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core erasterids; lamiids; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone can be obtained from the Univer Institute. Orders can be made through URL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The Institute for Genomic Research 9712 Medical Center Dr, Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Solanum tuberosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://genome.arizona.edu/orders/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: potato-array@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Solanum tuberosum (potato)
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                                                                                                                                                                                                                                              /clone_lib-"potato microtubers, in vitro-grown"
/clone_lib-"potato microtubers, in vitro-grown"
/note-"vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; Tissue supplied by Christian Bachem and Richard
Visser (Department of Plant Breeding, Wageningen
University, The Netherlands); sequencing by The Institute
for Genomic Research. The cSTA libraries will attempt to
capture the induction and initiation/initial growth of the
tuber in an in vitro system as described in Bachem et al.
(Plant Journal, 1996). Small microtubers develop from
axillary buds attached to stem explants when placed on a
high sucrose medium (10%). Visible morphological changes
occur synchronously at day five in the axillary buds. The
first library, cSTA (1-20) consists of axillary buds
harvested on days 1-3. This targets those genes involved
in induction of the microtubers. The following libraries,
cSTA (21-40) and cSTA (41-60), capture genes involved in
tuber initiation and outgrowth. This library is noted as
p3 in Tanksley lab notebooks."
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sink-tubers"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/cultivar="Bintje"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="cSTE26D20"
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   5.01e-26
315.50
55.85%
39.36%
16.91%
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Matches:
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hiemingo,A., Bougri,O.,
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70 99

Alignment Scores: 1.32e-25 Length: 720 Pred. No.: 313.00 Matches: 67	/db_xref_P(taxon:47834" /clone="PH_05.x" pt_05.x" /clone_1\(\bar{b}\bar{b}\) = "5ptroplasma kunkelii H" BASE COUNT 255 a 96 0 132 g 233 t 4 others ORIGIN	source 1720 /organism="Spiroplasma kunkelii" /mol_type="genomic DNA" /strain="M2"	Fax: 330 263 Email: hoger Class: Hindl	Department of Entomology The Ohio State University-OARDC 120 Thorne Hall, 1680 Madison Avenue, Wooster, OH 44691, USA Tel: 330 263 3730	AUTHORS Hogenhout, S.A. TITLE Genomic sequences from Spiroplasma kunkelii strain M2 JOURNAL Unpublished COMMENT Contact: Hogenhout SA	SÖURCE Spiroplasma kunkeliji ORGANISM Spiroplasma kunkeliji Bacteria; Firmicutes; Mollicutes; Entomoplasmatales; Spiroplasmataceae; Spiroplasma REFERENCE 1 (bases 1 to 720)		Sia .	Qy 233 GlyAspThrLeuArgValserLeu 240	Oy 213 AlaArgSerGlyAlaValLysSerAlaIleGlyLeuGlyLeuLeuLeuSerGluGlyIle 232	Qy 198 GlnIle	Qy 178 ValSerValLysAlaSerAspValPheLeuAlaValGluSerTyrArgLeuLeuAlaLys 197 :::	Qy 158 LeuGluSeralaMetArgHisValAspHisLeuAspArgLeuAsnPheAspGlnPheLys 177 ::: Db 305 GTAGAATCAGCATTTGAGTTTGCAAGAATTTGTAGAAAGTTTGGACTTTCACAATTTCGTC 364	Qy 138 AlaGlySerLeuGlubysAspLeuGlnGluLysTyrGlyGluProThrProGlnAlaLeu 157 :: ::: ::: ::: ::: Db 248 CATGGGAGCCCTTCAGATCGCATTATGAGCTATTATGGGGACTCGCCTAGGGGAATG 304	Qy 118 IleArgMetValValAspCysAlaArgAspLysAsnIleProIleArgIleGlyValAsn 137 ::: 38: :::	Db 128 GAGCAATTAGAGTACAGAAGATGACTATCAGAAAGAACTCGAGCATATTGAGGAGGTT 187	Db 71 TGCTTTGACAAAATACGTGTCAATCCTGGAAACTTTGCTGACAGGCGAGCCCAGTTT 127 Oy 115
/mol_type="genomic DNA" /strain="Salvador I (Collins, W. 1972. J. Parasitol. 69, 497-598)"	l: da prime s: sh	f Florida Avenue, Bldg 101 4700 9704		complexa; Haemosporida; Plasm J.B.		RESULT 8 AZ570993/c AZ570993/c AZ570993	Oy 349 UALBARGILE 352 Db 510 ACTATTAATT 519	329 uTyrGluAspo	Qy 310 -ProGlyGluAlaLeuValSerThrLeuGlyValThrGlyGlyAsnLysLysSerGlyLe 329	Qy 290 ArgLeuGluAspIleIleThrProMetAspValSerIleIleGlyCysValValAsnGly 309 ::: ::: ::: ::: ::: :::: ::: :	Qy 270 CysProThrCysSerargGlnGluPheAspVallleGlyThrValAsnAlaLeuGluGln 289	Qy 250 ValGlyPheAspIleLeuLysSerLeuArgIleArgSerArgGlyIleAsnPheIleAla 269 ::: ::: Db 210 GTTGGTAAACGAATGTTAAATTCATTAGGACTTTATGATAACATTGTTGATATAATTGCT 269	Qy. 230 GluGlyIleGlyAspThrLeuArgValSerLeuAlaAlaAspProValGluGluIleLys 249	Qy 210 AlaGlyGlyAlaArgSerGlyAlaValLysSerAlaIleGlyLeuGlyLeuLeuSer 229	Qy 190 GluSerTyrArgLeuLeuAlaLysGlnIleAspGlnProLeuHisLeuGlyIleThrGlu 209 :::::: ::: ::::	US-09-921-992-78 (1-372) x BH235010 (1-720)	Percent Similarity: 62.20% Conservative: 35 Best Local Similarity: 40.85% Mismatches: 61 Query Match: 16.77% Indels: 2 DB: 28 Gaps: 0

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Percent Similarity:
Best Local Similarity:
Query Match:
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AlaIleGlyLeuGlyLeuLeuLeuSerGluGlyIleGlyAspThrLeuArgValSerLeu
                                                                                                                                                ATACAGTCGTATAGGCTACTCGTGGCGAGGCAATATGAAAGGATGGGCAACGGGTTACTA 172
                                                                                                                                                                                                                                               GTACAGAATAACTTCTTCAATGTGGTTTTCTCCATGAAGGCTTCCAACGCGTATATAATG
                                                TTCCCACTGCATTTGGGCGTTACCGAAGCAGGGTTTGGGGGATAACGGAAGGATAAAATCC
                                                                             ---ProLeuHisLeuGlyIleThrGluAlaGlyGlyAlaArgSerGlyAlaValLysSer
                                                                                                                                                                       AspArgLeuAsnPheAspGlnPheLysValSerValLysAlaSerAspValPheLeuAla 188
                                                                                                                                                                                                                                                                                                                                                                                                                                           AATAGAGCCATACGAATCGGCACAAATCACGGCTCCCTATCTTNTAGGGTACTCTCTTTC 349
                                                                                                                                                                                                                                                                                                                                            TATGGGGAT---ACCCCNTTAGGTATGGTCGAATCGGCGTTTGAATTTTCCGATTTGTGT 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGAAATTATTTATTCAGNAGAAGTTCATCCCCTTGATTGAAAAGTGTAAGAGG---TTA 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTCGATGGGAGNAAGAATGGATCAATAAGATTTACAAAACGAGAGAAGANTTCGATCAA 466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AsnīleProīleArgīleGlyValAsnAlaGlySerLeuGluLysAspLeuGlnGluLys 148
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150 c 119 g
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/lab_host="Saimiri boliviensis"
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1 (bases 1 to 852)

1 (bases 1 to 852)

Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E. Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G. Large-scale identification of ESTs involved in the interaction
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BACKWARD: gga aac agc tat gac cat g
Plate: 04 row: B column: 06
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Fax: 520 621 9288
Email: http://genome.arizona.edu
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University of Arizona
Biological Sciences W
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Oryza sativa (indica cultivar-group)
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/Clome_lib="OSIIEb"
/clome_Tyector: pBluescript II KS +; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
/note="Yector: pBluescript II KS +; Site_1: EcoRI; Site_2:
/note="Vector: pbluescript II KS +; Site_1: EcoRI; Site_2: EcoRI; EcoRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Oryza sativa (indica cultivar-group)"
/mol_type="mRNA"
/cultivar="IR36"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="Leaf"
/dev_stage="3 week"
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Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CA022320.1
                                                                                                                                                                                                                                                           Email: stein@ipk-gatersleben.de
Insert Length: 602 Std Error:
Plate: 42 row: M column: 11
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Tel: 039482-5522
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Institute of Plant Genetics and Crop Plant Research
Corrensstr. 3, 06466, Gatersleben, Germany
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Radchuk, V., Zhang, H., Weschke, W.,
Barley ESTs from developing seeds
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                                        /db_xref="taxon:112509"
/clone="HZ42M11"
                                                                                                                                                                                               Location/Qualifiers
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/tissue_type="pericarp"
/dev_stage="0-7 DAP (days after
                                                                                                                 /cultivar="barke"
                                                                                     /db_xref="GABI:275726"
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US-09-921-992-78 (1-372) \times CA022320
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Best Local Similarity:
BJ481080 610 bp mRNA linear EST 23-MAY-2002 BJ481080 K. Sato unpublished cDNA library, strain H602 adult, heading stage top three leaves Hordeum vulgare subsp. spontaneum cDNA clone bah58i01 5', mRNA sequence.
BJ481080. GI:21159548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGCGCTGATTTTGTTAGAATAACCGTCCAGGGTAAAAAAGGAAGCTGATGCCTGCTTTGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlyAsnIleGlyAsnGlu---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AspTyrArgIleAlaLeuLysValAlaGluTyrGlyValAspCysLeuArgIleAsnPro 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTAAGAACACTCTTGTCCAGAAGAATTACAACATCCCTCTAGCGGCCGATATCCATTTT
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//clone_lib="HZ"
//clone_lib="HZ"
//clone_lib="HZ"
//clone_lib="HZ"
//clone_lib="HZ"
//clone_lib="HZ"
//clone_lib="HZ"
//clone="Yector: pBluescript SK+; Site_1: EcoRI (5'-end of //clone); Site_2: XhoI (3'-end of cDNA); pericarp 0-7

DAP(days after pollination). Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRIAdapter used for cloning. To excise the insert, restriction sites upstream EcoRI should excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, Sall, Pstl). NOTE: Also due to the cloning system used Blue/white selection for recombinats is not 100% reliable.Average insert size is 900 bp"
69 a 110 c 156 g 167 t
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                                                                                                                                                                                                                                                                                                                                                58 IleValArgValSerValProThrMetAspAlaAlaGluAlaPhe-------
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Hordeum vulgare subsp. spontaneum
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540,
Tel: 81-559-81-6856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sato, K., Saisho, D. and Takeda, K. Barley EST sequencing project in
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                                                                                                                                                                                                                                                                                                                   TTTGTTAGAATAACCGTCCAGGGTAAAAAGGAAGCTGATGCCTGCTTTGAGATTAAGAAC
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                                                                                                                                                                       GlyAsnGlu-----
                                                                                                                                                                                                                             IleAlaLeuLysValAlaGluTyrGlyValAspCysLeuArgIleAsnProGlyAsnIle 112
                                                                                                                                                                                                                                                                                                                                                                            GluProThrProGlnAlaLeuLeuGluSerAlaMetArgHisValAspHisLeuAspArg 170
                                                       ProlleArglleGlyValAsnAlaGlySerLeuGluLysAspLeuGlnGluLysTyrGly 150
                                                                                                              ---GluArgIleArgMetVal------ValAspCysAlaArgAspLysAsnIle 130
                                                                                                                                            GCCGATCGCCGTGCCCAATTTGAAAAGCTGGAATATACTGAAGACGATTACGAAAAGGAG
                                                                                                                                                                                                     GTAGCTTTAAGAGTGGCTGAATGC---TTTGACAAAATCCGTGTTAACCCAGGAAACTTT 306
                            GCCATGCGTATCGGAACAAATCATGGTAGTCTTTCTGACCGGATAATGAGCTACTATGGT
                                                                                   CTTGAACACATTGAGAGGGTCTTTTCTCCATTGGTTGAGAAATGCAAGAAGTATGGAAGA
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Location/Qualifiers
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/db_xref**taxon:77009"
/db_xref**taxon:77009"
/clone="bah59101"
/tissue_type="top three leaves"
/dev_stage="adult, heading stage"
/clone_lib**K. Sato unpublished cDNA library,
adult, heading stage top three leaves"
a 118 c 155 g 160 t 1 others
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269.50
51.49%
33.66%
14.44%
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UŚ-09-921-992-78 (1-372) x BG591263
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Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum.
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                                      "COMPARISON OF RNA EXPRESS PORPHYRA YEZOENSIS (RHODOE) ANALYSIS";
                                J. Phycol. 0:0-0(2003).
                                                                                                               Submitted (15-JUN-2001) to the EMBL/GenBank/DDBJ databases. Erika Asamizu, Kazusa DNA Research Institute, The First Laboratory f Plant Gene Research; 15323 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:asamizu@kazusa.of.)]p, URL:http://www.kazusa.or.]p/en/plant/, Tel:81-438-52-3935(ex.2336), Fax:81-438-52-3934)
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/strain="TU-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 A; 136
                                      ta; Coniferopsida;
to 601)
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                           Kinlaw, C.S., Retzel, E.
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Sederoff, R.R.

Tracheophyta; Pinus; Pinus.

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             BJ551332 K. Sato unpublished cDNA library, strain H602 adult, heading stage top three leaves Hordeum vulgare subsp. spontaneum BJ551332
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North Carolina State University
Dept. of Forestry, NC State University, 6113 Jordan Hall, Raleigh
NC, 27695-8008
                                                                                                                                                           GTTACTGAAGCTGGTGAAGGTGAAGATGGACGCATGAAGTCTGCAATTGGCATTGGAACA
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Seq primer: 5' lambda TriplEx2 Sequencing
                                                                                                                  GAGATC
                                                                                                                                         GluIle 248
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/mol_type="mRNA"
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/note="Organ: shoot tips; Vector: Lambda TriplEx; Site_1:
Sfi1 (A); Site_2: Sfi1 (B); Shoot tips (approx. 2 cm from apex) were collected during the spring, frozen and used for mRNA isolation. The SMART-PCR method (Clontech) was used to prepare a library from 1 ug total RNA, using the Lambda TriplEx vector. Plasmid subclones in pTriplEx were recovered by cre-lox excision in E. coli strain BM25.8 and 103 c 166 g 165 t 5 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
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Sato,K., Saisho,D. and Takeda,K.
Barley EST sequencing project in NIG
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldea
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                GluIle 248
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                                                 CTTTTGATGGATGGCTTGGGTGATACAATCCGTGTATCCCTCACAGAACCACCAGAGGAA
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                                                                  GTTACCGAAGCTGGTGAGGGTGAAGATGGGAGGATGAAGTCTGCTATTGGCATCGGAACA
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Location/Qualifiers
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adult, heading stage top three leaves"
adult, heading stage top three leaves
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/mol_type="mRNA"
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Result
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1 MHNQAPIQRRKSTRIYVGNV......RAKASQLDEARRIDVQQVEK 372
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Copyright (c) 1993 - 2003 Compugen Ltd.
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O8dez8 vibrio vuln
O8ec32 shewanella
O8dly3 wiggleswort
O89796 bifidobacte
O8fp82 corynebacte
O8eu16 mycoplasma
O8dk70 synechococc
O8f1h5 leptospira
O8fyt2 brucella su
O8gzr6 lycopersico
O8rxg8 arabidopsis
O9ff59 arabidopsis
O8lp44 arabidopsis
O8lp44 arabidopsis
O8kg23 chlorobium
O9bjx5 plasmodium
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Q8EC32;
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Q1-MAR-2003 (TEMBLrel. 23) Last sequence update)
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             Q8G7Y6 PRELIMINARY; PRT; 403 AA.
Q8G7Y6;
Q1-MAR-2003 (TrEMBLrel. 23, Created)
Q1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Q8D1Y3;
01-MAR-2003 (TrEMBLrel. 2
01-MAR-2003 (TrEMBLrel. 2
01-MAR-2003 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wigglesworthia brevipalpis.
Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Wigglesworthia.
NCBI_TaxID=164609;
                                                                                                                                                                                                                                                                                                                                                                                                                                 flies, Wigglesworthia glossinidia.";
Nat. Genet. 32:402-407(2002).
EMBL; AB063522; BAC24719.1;
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Best Local S
Matches 167
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OBFPB2;
O1-MAR-2003 (TIEMBLIEL 2
01-MAR-2003 (TIEMBLIEL 2
01-MAR-2003 (TIEMBLIEL 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Actinobacteridae; Bifidobacteridae; Bifidobacteriaceae; Bifidobacterium. NCBI_TaxID=216816;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ISPG OR BL0098.
Bifidobacterium
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MEDLINE=22294977; PubMed=12381787;
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                                           SEQUENCE FROM N.A.

STRAIN-YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
STRAIN-YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
Kawarabayasi Y., Yamazaki J., Hino Y., Kikuchi H.,
Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi
Usuda Y., Sugimoto S.;
                                                                                                                                                                   Corynebacterium efficiens.

Bacteria; Actinobacteria; Actinobacteridae; Actinomycet
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBI_TaxID=152794;
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      "The entire
Submitted (M
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Pred. No. 4.2e
70; Mismatches
  of Corynebacterium efficient EMBL/GenBank/DDBJ databases
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Shimpo S., Sugimoto M.,
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Kiyokawa C.,
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Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J., Baugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Vran Ak Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L. Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C. "The Brucella suis genome reveals fundamental similarities bet animal and plant pathogens and symbionts.", proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
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STRAIN-1330 / Blovar 1;
MEDLINB-22247741; PubMed-12271122;
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Q8GZR6;
Q1-MAR-2003
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                                                                                                                                                                                                                                                              Submitted (CCT-2001) to the EMBL/GenBank/DDBJ databases EMBL; AF435086; AA015447.1; - 8668C9F08078FA05 CRC64;
                                                                                                                                                                                                                                                                                                                                                Escherichia coli gcpE gene
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
Asteridae; lamiids; Solanales; Solanaceae; Solanum.
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                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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TIGR;
Comple
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BR1778; -.
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                   ADACFEIKNTLVQKNYNIPLVADIHFAPSVALRVAEC-FDKIRVNPGNFADRRAQFEQLE
                                               RRQTCTVMVGNVALGSEHPIRIQTMTTTDTKDVAATVEQVMKIADAGADIVRITVQGRKE
                                                                                                                          RRKSTRIYVGNVPIGDGAPIAVQSMTNTRTTDVEATVNQIKALERVGADIVRVSVPTMDA
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                                                                                                                                                                                        25.2%; Score 471; ilarity 40.1%; Pred. No. 2 Conservative 45; Mismatch
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Pred. No. 2
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Matches 105; Conserv
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SEQUENCE FROM N.A.

Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M.,

Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,

Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai

Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,

Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,

Ecker J., Theologis A., Davis R.W.;

Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AY081261; AAL91150.1;
                                                                                                                                                                                                                                                                                                              InterPro; IPR004588; IspG.
InterPro; IPR004588; IspG.
Pfam; PF04551; GcpE; 1.
TICRFAMs; TIGR00612; IspG_gcpE;
SEQUENCE 741 AA; 82157 MW; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-JUN-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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AT5G60600.
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                       AVKSAIGLGLLLSEGIGDTLRVSLAADPVEEI
                                              FEFARICRKLDYHNFVFSMKASNPVIMVQAYRLLVAEMYVHGWDYPLHLGVTEAGEGEDG
                                                                       MRHVDHLDRLNFDQFKVSVKASDVFLAVESYRLLAKQI-----DQPLHLGITEAGGARSG
                                                                                                 YTEDEYQKELQHIEQVFTPLVEKCKKYGRAMRIGTNHGSLSDRIMSYYGD-SPRGMVESA
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Q9FF59; Q9FF59; 01-MAR-2001

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Matches 105
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Arabidopsis thaliana (Mouse ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eparatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Miyajima N., Tabata S.;
"Structural analysis of Ar
features of the 1.6 Mb reg
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SEQUENCE
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01-MAR-2003
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01-MAR-2003
01-MAR-2003
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STRAN-Columbia;
MEDLINE-97471969; PubMed-9330910;
Watani H., Nakamuga Y., Kaneko T.,
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                                                                                                   Querol J., Campos N., Imperial S., BOLOU
Rodriguez-Concepcion M.;
"Identification and functional analysis
Escherichia coli gcpE gene product with
                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; 
Spermatophyta; Magnolioph 
eurosids II; Brassicales;
                                                                                                                                                                                                                                                                                                                                                                                                Q8GZR7
                                                                     biosynthesis.";
submitted (OCT-)
                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                  NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Mou
                                                                                                                                                                                                                                                                                                                             01-MAR-2003
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AB005246; BAB09833.Lg.-

ABPTO; IPR004588; ISPG

APAMS; TIGR00612; ISPG-GCPE;

JENCE 716 AA; 79817 MW; 28
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                                   AF434673;
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AAO15446 11:
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38.6%
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230
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                                                                                                                                                       perial S.,

    BG-ear cress).
    Streptophyta; Embryophyta; Tracheophyta;
    Dyka; eudicotyledons; core eudicots; Rosid
    Brassicaceae; Arabidopsis.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ESMKASNPVIMVQAYRLLVAEMYVHGWDYPLHLGVTEAGEGEDG
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                                           ΨW.
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                                                                           EMBL/GenBank/DDBJ
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                                           8EF625E9A9C88074
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     Length 740
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ID Q8LPQ4
OBLPC
DT 01-00
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OC Euka
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RN (11)
RP SEQ
RA Shi
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Best Local Similarity Matches 105; Conser
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosideurosids II. Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shinn P., Chen H., Cheuk R., Kim C.J., Meyers M.C., Banh J., Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D., Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Sat Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada R. Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2002 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                            Interpro; IPRO06705; GCDE.
Interpro; IPRO04588; ISpG.
Pfam; PF04551; GCDE; 2.
TIGREAMS; TIGRO0612; ISpG.gcpE;
SEQUENCE 741 AA; 82257 MW; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AY094472; AAM19840.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Arabidopsis cDNA clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AVKSAIGLGLLLSEGIGDTLRVSLAADPVEEI 248
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                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                     RRKSTRIYVGNVPIGDGAPIAVQSMTNTRTTDVEATVNQIKALERVGADIVRVSVPTMDA
                                                                                CARDK
MRHVDHLDRLNFDQFKVSVKASDVFLAVESYRLLAKQI--
                                                                                                                    ADACFEIKDKLVQLNYNIPLVADIHFAPTVALRVAEC-FDKIRVNPGNFADRRAQFETID
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                                                                                                                                                                                                                                                                                      48;
                                                                                                                                                                                                                                                                                Score 457; DB
Pred. No. 2.9e
48; Mismatches
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Last annotation updat
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7; Mismatches
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                                                                                                                                                                                                                                                                                                         457; DB 10;
No. 2.9e-25;
                                                                              -NIPIRIGVNAGSLEKDLQEKYGEPTPQALLESA
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                                                                                                                                                                                                                                                                                                                              Length 741;
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        -DQPLHLGITEAGGARSG
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(C STRAIN-TLS / ATCC 49652 / DSM 12025;

(X MEDLINE-2210368; PubMed-12093901;

(A Elsen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,

(A Dodson R.J., Deboy R., Gwinn M.L., Nelson W.C., Haft D.H.,

(A Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F.,

(A Holt I., Umayam L.A., Mason T., Brenner M., Shea T.P., Parksey D.,

(A Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune D.,

(A Vanathevan J., Khouri H., White O., Gruber T.M., Ketchum K.A.,

(A Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.;

(A Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.;

(The complete genome sequence of Chlorobium tepidum TLS, a Photosynthetic, anaerobic, green-sulfur bacterium.";

(Proc. Natl. Acad. Scil. U.S.A. 99:9509-9514(2002).
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Best Local Similarity
Matches 108; Conserv
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Complete proteome.
SEQUENCE 746 AA; 82087 MW; B40ED95B6010C5F9 CRC64;
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TIGR; CT01147;
InterPro; IPR006705; GcpE.
InterPro; IPR004588; IspG.
Pfam; PF04551; GcpE; 2.
TIGREAMS; TIGR00612; IspG_9cpE; 1.
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01-OCT-2002
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GCPE OR CT0147.
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Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
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                                                                                                                                                 156 ALLESAMRHVDHL-DRLNFDQFKVSVKASDVFLAVESYRLLAKQID-----QPLHLGIT 208
                                                                                                                                                                                187 KFSSKDYTDDEYRAELDKVREEFTPLVRKARSLGVSMRIGTNHGSLSDRIVSRYGN-SPE 245
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